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Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile
 770 775 780
 Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
 785 790 795 800
 Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
 805 810 815
 Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln
 820 825 830
 Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
 835 840 845
 Ile Lys Glu Asn Thr Gly Val
 850 855

<210> 3
 <211> 2137
 <212> DNA
 <213> Homo Sapien

<220>
 <221> CDS
 <222> (261)...(1574)
 <223> Nucleic acid encoding a transmembrane serine
 protease (MTSP3) protein

<400> 3
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 agcagcttgc tcagcggaca aggatgctgg gcgtgagggga ccaaggcctg ccctgcactc 120
 gggcctcctc cagccagtgc tgaccaggga cttctgacct gctggccagc caggacctgt 180
 gtggggagggc cctcctgctg ccttgggggtg acaatctcag ctccaggcta caggagagacc 240
 gggaggatca cagagccagc atg tta cag gat cct gac agt gat caa cct ctg 293
 Met Leu Gln Asp Pro Asp Ser Asp Gln Pro Leu
 1 5 10
 aac agc ctc gat gtc aaa ccc ctg cgc aaa ccc cgt atc ccc atg gag 341
 Asn Ser Leu Asp Val Lys Pro Leu Arg Lys Pro Arg Ile Pro Met Glu
 15 20 25
 acc ttc aga aag gtg ggg atc ccc atc atc ata gca cta ctg agc ctg 389
 Thr Phe Arg Lys Val Gly Ile Pro Ile Ile Ile Ala Leu Leu Ser Leu
 30 35 40
 gcg agt atc atc att gtg gtt gtc ctc atc aag gtg att ctg gat aaa 437
 Ala Ser Ile Ile Ile Val Val Leu Ile Lys Val Ile Leu Asp Lys
 45 50 55
 tac tac ttc ctc tgc ggg cag cct ctc cac ttc atc ccg agg aag cag 485
 Tyr Tyr Phe Leu Cys Gly Gln Pro Leu His Phe Ile Pro Arg Lys Gln
 60 65 70 75
 ctg tgt gac gga gag ctg gac tgt ccc ttg ggg gag gac gag gag cac 533
 Leu Cys Asp Gly Glu Leu Asp Cys Pro Leu Gly Glu Asp Glu Glu His
 80 85 90
 tgt gtc aag agc ttc ccc gaa ggg cct gca gtg gca gtc cgc ctc tcc 581
 Cys Val Lys Ser Phe Pro Glu Gly Pro Ala Val Ala Val Arg Leu Ser
 95 100 105
 aag gac cga tcc aca ctg cag gtg ctg gac tgg gcc aca ggg aac tgg 629
 Lys Asp Arg Ser Thr Leu Gln Val Leu Asp Ser Ala Thr Gly Asn Trp
 110 115 120

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ttc tct gcc tgt ttc gac aac ttc aca gaa gct ctc gct gag aca gcc Phe Ser Ala Cys Phe Asp Asn Phe Thr Glu Ala Leu Ala Glu Thr Ala 125 130 135	677
tgt agg cag atg ggc tac agc agc aaa ccc acc ttc aga gct gtg gag Cys Arg Gln Met Gly Tyr Ser Ser Lys Pro Thr Phe Arg Ala Val Glu 140 145 150 155	725
att ggc cca gac cag gat ctg gat gtt gtt gaa atc aca gaa aac agc Ile Gly Pro Asp Gln Asp Leu Asp Val Val Glu Ile Thr Glu Asn Ser 160 165 170	773
cag gag ctt cgc atg cgg aac tca agt ggg ccc tgt ctc tca ggc tcc Gln Glu Leu Arg Met Arg Asn Ser Ser Gly Pro Cys Leu Ser Gly Ser 175 180 185	821
ctg gtc tcc ctg cac tgt ctt gcc tgt ggg aag agc ctg aag acc ccc Leu Val Ser Leu His Cys Leu Ala Cys Gly Lys Ser Leu Lys Thr Pro 190 195 200	869
cgt gtg gtg ggt ggg gag gag gcc tct gtg gat tct tgg cct tgg cag Arg Val Val Gly Gly Glu Glu Ala Ser Val Asp Ser Trp Pro Trp Gln 205 210 215	917
gtc agc atc cag tac gac ata cag cac gtc tgt gga ggg agc atc ctg Val Ser Ile Gln Tyr Asp Ile Gln His Val Cys Gly Gly Ser Ile Leu 220 225 230 235	965
gac ccc cac tgg gtc ctc acg gca gcc cac tgc ttc agg aaa cat acc Asp Pro His Trp Val Leu Thr Ala Ala His Cys Phe Arg Lys His Thr 240 245 250	1013
gat gtg ttc aac tgg aag gtg cgg gca ggc tca gac aaa ctg ggc agc Asp Val Phe Asn Trp Lys Val Arg Ala Gly Ser Asp Lys Leu Gly Ser 255 260 265	1061
ttc cca tcc ctg gct gtg gcc aag atc atc atc att gaa ttc aac ccc Phe Pro Ser Leu Ala Val Ala Lys Ile Ile Ile Ile Glu Phe Asn Pro 270 275 280	1109
atg tac ccc aaa gac aat gac atc gcc ctc atg aag ctg cag ttc cca Met Tyr Pro Lys Asp Asn Asp Ile Ala Leu Met Lys Leu Gln Phe Pro 285 290 295	1157
ctc act ttc tca ggc aca gtc agg ctc atc tgt ctg ccc ttc ttt gat Leu Thr Phe Ser Gly Thr Val Arg Leu Ile Cys Leu Pro Phe Phe Asp 300 305 310 315	1205
gag gag ctc act cca gcc acc cca ctc tgg atc att gga tgg ggc ttt Glu Glu Leu Thr Pro Ala Thr Pro Leu Trp Ile Ile Gly Trp Gly Phe 320 325 330	1253
acg aag cag aat gga ggg aag atg tct gac ata ctg ctg cag gcg tca Thr Lys Gln Asn Gly Gly Lys Met Ser Asp Ile Leu Leu Gln Ala Ser 335 340 345	1301
gtc cag gtc att gac agc aca cgg tgc aat gca gac gat gcg tac cag Val Gln Val Ile Asp Ser Thr Arg Cys Asn Ala Asp Asp Ala Tyr Gln 350 355 360	1349
ggg gaa gtc acc gag aag atg atg tgt gca ggc atc ccg gaa ggg ggt	1397

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Gly Glu Val Thr Glu Lys Met Met Cys Ala Gly Ile Pro Glu Gly Gly
 365 370 375

gtg gac acc tgc cag ggt gac agt ggt ggg ccc ctg atg tac caa tct 1445
 Val Asp Thr Cys Gln Gly Asp Ser Gly Gly Pro Leu Met Tyr Gln Ser
 380 385 390 395

gac cag tgg cat gtg gtg ggc atc gtt agc tgg ggc tat ggc tgc ggg 1493
 Asp Gln Trp His Val Val Gly Ile Val Ser Trp Gly Tyr Gly Cys Gly
 400 405 410

ggc ccg agc acc cca gga gta tac acc aag gtc tca gcc tat ctc aac 1541
 Gly Pro Ser Thr Pro Gly Val Tyr Thr Lys Val Ser Ala Tyr Leu Asn
 415 420 425

tgg atc tac aat gtc tgg aag gct gag ctg taa tgctgtgtgcc cctttgcagt 1594
 Trp Ile Tyr Asn Val Trp Lys Ala Glu Leu *
 430 435

gctgggagcc gcttccttcc tgcctgtccc acctggggat ccccccaggc cagacacaga 1654
 gcaagagtcc ccttgggtac acccctctgc ccacagcctc agcatttctt ggagcagcaa 1714
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 ccttagctcg gccacacttg gtgtctccag catcccaggg agagacacag cccactgaac 1834
 aaggtctcag gggatttgct aagccaagaa ggaactttcc cacactactg aatggaagca 1894
 ggctgtcttg taaaagccca gatcactgtg ggctggagag gagaaggaaa ggtctgtcgc 1954
 cagccctgtc cgttttcacc catccccaag cctactagag caagaaacca gttgtaatat 2014
 aaaatgcact gccctactgt tggatgact accgttacct actgttgtca ttgttattac 2074
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 aaa 2137

<210> 4
 <211> 437
 <212> PRT
 <213> Homo Sapien

<400> 4
 Met Leu Gln Asp Pro Asp Ser Asp Gln Pro Leu Asn Ser Leu Asp Val
 1 5 10 15
 Lys Pro Leu Arg Lys Pro Arg Ile Pro Met Glu Thr Phe Arg Lys Val
 20 25 30
 Gly Ile Pro Ile Ile Ile Ala Leu Leu Ser Leu Ala Ser Ile Ile Ile
 35 40 45
 Val Val Val Leu Ile Lys Val Ile Leu Asp Lys Tyr Tyr Phe Leu Cys
 50 55 60
 Gly Gln Pro Leu His Phe Ile Pro Arg Lys Gln Leu Cys Asp Gly Glu
 65 70 75 80
 Leu Asp Cys Pro Leu Gly Glu Asp Glu Glu His Cys Val Lys Ser Phe
 85 90 95
 Pro Glu Gly Pro Ala Val Ala Val Arg Leu Ser Lys Asp Arg Ser Thr
 100 105 110
 Leu Gln Val Leu Asp Ser Ala Thr Gly Asn Trp Phe Ser Ala Cys Phe
 115 120 125
 Asp Asn Phe Thr Glu Ala Leu Ala Glu Thr Ala Cys Arg Gln Met Gly
 130 135 140
 Tyr Ser Ser Lys Pro Thr Phe Arg Ala Val Glu Ile Gly Pro Asp Gln
 145 150 155 160
 Asp Leu Asp Val Val Glu Ile Thr Glu Asn Ser Gln Glu Leu Arg Met
 165 170 175
 Arg Asn Ser Ser Gly Pro Cys Leu Ser Gly Ser Leu Val Ser Leu His
 180 185 190
 Cys Leu Ala Cys Gly Lys Ser Leu Lys Thr Pro Arg Val Val Gly Gly

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      195      200      205
Glu Glu Ala Ser Val Asp Ser Trp Pro Trp Gln Val Ser Ile Gln Tyr
210      215      220
Asp Ile Gln His Val Cys Gly Gly Ser Ile Leu Asp Pro His Trp Val
225      230      235      240
Leu Thr Ala Ala His Cys Phe Arg Lys His Thr Asp Val Phe Asn Trp
      245      250      255
Lys Val Arg Ala Gly Ser Asp Lys Leu Gly Ser Phe Pro Ser Leu Ala
260      265      270
Val Ala Lys Ile Ile Ile Ile Glu Phe Asn Pro Met Tyr Pro Lys Asp
275      280      285
Asn Asp Ile Ala Leu Met Lys Leu Gln Phe Pro Leu Thr Phe Ser Gly
290      295      300
Thr Val Arg Leu Ile Cys Leu Pro Phe Phe Asp Glu Glu Leu Thr Pro
305      310      315      320
Ala Thr Pro Leu Trp Ile Ile Gly Trp Gly Phe Thr Lys Gln Asn Gly
      325      330      335
Gly Lys Met Ser Asp Ile Leu Leu Gln Ala Ser Val Gln Val Ile Asp
340      345      350
Ser Thr Arg Cys Asn Ala Asp Asp Ala Tyr Gln Gly Glu Val Thr Glu
355      360      365
Lys Met Met Cys Ala Gly Ile Pro Glu Gly Gly Val Asp Thr Cys Gln
370      375      380
Gly Asp Ser Gly Gly Pro Leu Met Tyr Gln Ser Asp Gln Trp His Val
385      390      395      400
Val Gly Ile Val Ser Trp Gly Tyr Gly Cys Gly Gly Pro Ser Thr Pro
      405      410      415
Gly Val Tyr Thr Lys Val Ser Ala Tyr Leu Asn Trp Ile Tyr Asn Val
420      425      430
Trp Lys Ala Glu Leu
435

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<210> 5

<211> 708

<212> DNA

<213> Homo Sapien

<220>

<221> CDS

<222> (1)...(708)

<223> Nucleic acid encoding an MTSP4 protease domain

<400> 5

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att gtt ggt gga gct gtg tcc tcc gag ggt gag tgg cca tgg cag gcc      48
Ile Val Gly Gly Ala Val Ser Ser Glu Gly Glu Trp Pro Trp Gln Ala
1      5      10      15

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agc ctc cag gtt cgg ggt cga cac atc tgt ggg ggg gcc ctc atc gct      96
Ser Leu Gln Val Arg Gly Arg His Ile Cys Gly Gly Ala Leu Ile Ala
      20      25      30

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gac cgc tgg gtg ata aca gct gcc cac tgc ttc cag gag gac agc atg      144
Asp Arg Trp Val Ile Thr Ala Ala His Cys Phe Gln Glu Asp Ser Met
      35      40      45

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```

gcc tcc acg gtg ctg tgg acc gtg ttc ctg ggc aag gtg tgg cag aac      192
Ala Ser Thr Val Leu Trp Thr Val Phe Leu Gly Lys Val Trp Gln Asn
      50      55      60

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tcg cgc tgg cct gga gag gtg tcc ttc aag gtg agc cgc ctg ctc ctg      240
Ser Arg Trp Pro Gly Glu Val Ser Phe Lys Val Ser Arg Leu Leu Leu

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65	70	75	80	
cac ccg tac cac gaa gag gac agc cat gac tac gac gtg gcg ctg ctg				288
His Pro Tyr His Glu Glu Asp Ser His Asp Tyr Asp Val Ala Leu Leu	85	90	95	
cag ctc gac cac ccg gtg gtg cgc tgc gcc gcc gtg cgc ccc gtc tgc				336
Gln Leu Asp His Pro Val Val Arg Ser Ala Ala Val Arg Pro Val Cys	100	105	110	
ctg ccc gcg cgc tcc cac ttc ttc gag ccc gcc ctg cac tgc tgg att				384
Leu Pro Ala Arg Ser His Phe Phe Glu Pro Gly Leu His Cys Trp Ile	115	120	125	
acg gcc tgg gcc gcc ttg cgc gag gcc gcc ccc atc agc aac gct ctg				432
Thr Gly Trp Gly Ala Leu Arg Glu Gly Gly Pro Ile Ser Asn Ala Leu	130	135	140	
cag aaa gtg gat gtg cag ttg atc cca cag gac ctg tgc agc gag gtc				480
Gln Lys Val Asp Val Gln Leu Ile Pro Gln Asp Leu Cys Ser Glu Val	145	150	155	
tat cgc tac cag gtg acg cca cgc atg ctg tgt gcc gcc tac cgc aag				528
Tyr Arg Tyr Gln Val Thr Pro Arg Met Leu Cys Ala Gly Tyr Arg Lys	165	170	175	
ggc aag aag gat gcc tgt cag ggt gac tca ggt ggt ccg ctg gtg tgc				576
Gly Lys Lys Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys	180	185	190	
aag gca ctc agt gcc cgc tgg ttc ctg gcg ggg ctg gtc agc tgg gcc				624
Lys Ala Leu Ser Gly Arg Trp Phe Leu Ala Gly Leu Val Ser Trp Gly	195	200	205	
ctg gcc tgt gcc cgc cct aac tac ttc gcc gtc tac acc cgc atc aca				672
Leu Gly Cys Gly Arg Pro Asn Tyr Phe Gly Val Tyr Thr Arg Ile Thr	210	215	220	
ggt gtg atc agc tgg atc cag caa gtg gtg acc tga				708
Gly Val Ile Ser Trp Ile Gln Gln Val Val Thr *	225	230	235	

<210> 6

<211> 235

<212> PRT

<213> Homo Sapien

<400> 6

Ile Val Gly Gly Ala Val Ser Ser Glu Gly Glu Trp Pro Trp Gln Ala	1	5	10	15
Ser Leu Gln Val Arg Gly Arg His Ile Cys Gly Gly Ala Leu Ile Ala	20	25	30	
Asp Arg Trp Val Ile Thr Ala Ala His Cys Phe Gln Glu Asp Ser Met	35	40	45	
Ala Ser Thr Val Leu Trp Thr Val Phe Leu Gly Lys Val Trp Gln Asn	50	55	60	
Ser Arg Trp Pro Gly Glu Val Ser Phe Lys Val Ser Arg Leu Leu Leu	65	70	75	80
His Pro Tyr His Glu Glu Asp Ser His Asp Tyr Asp Val Ala Leu Leu	85	90	95	

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Gln Leu Asp His Pro Val Val Arg Ser Ala Ala Val Arg Pro Val Cys
 100 105 110
 Leu Pro Ala Arg Ser His Phe Phe Glu Pro Gly Leu His Cys Trp Ile
 115 120 125
 Thr Gly Trp Gly Ala Leu Arg Glu Gly Gly Pro Ile Ser Asn Ala Leu
 130 135 140
 Gln Lys Val Asp Val Gln Leu Ile Pro Gln Asp Leu Cys Ser Glu Val
 145 150 155 160
 Tyr Arg Tyr Gln Val Thr Pro Arg Met Leu Cys Ala Gly Tyr Arg Lys
 165 170 175
 Gly Lys Lys Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys
 180 185 190
 Lys Ala Leu Ser Gly Arg Trp Phe Leu Ala Gly Leu Val Ser Trp Gly
 195 200 205
 Leu Gly Cys Gly Arg Pro Asn Tyr Phe Gly Val Tyr Thr Arg Ile Thr
 210 215 220
 Gly Val Ile Ser Trp Ile Gln Gln Val Val Thr
 225 230 235

<210> 7

<211> 3104

<212> DNA

<213> Homo Sapien

<220>

<221> CDS

<222> (33)...(2441)

<223> Nucleic acid encoding MTSP4-L (long form) splice variant

<400> 7

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	Met Pro Val Ala Glu Ala Pro	
	1 5	
cag gtg gct ggc ggg cag ggg gac gga ggt gat ggc gag gaa gcg gag		101
Gln Val Ala Gly Gly Gln Gly Asp Gly Gly Asp Gly Glu Glu Ala Glu		
	10 20	
ccg gag ggg atg ttc aag gcc tgt gag gac tcc aag aga aaa gcc cgg		149
Pro Glu Gly Met Phe Lys Ala Cys Glu Asp Ser Lys Arg Lys Ala Arg		
	25 30 35	
ggc tac ctc cgc ctg gtg ccc ctg ttt gtg ctg ctg gcc ctg ctc gtg		197
Gly Tyr Leu Arg Leu Val Pro Leu Phe Val Leu Leu Ala Leu Leu Val		
	40 45 50 55	
ctg gct tcg gcg ggg gtg cta ctc tgg tat ttc cta ggg tac aag gcg		245
Leu Ala Ser Ala Gly Val Leu Leu Trp Tyr Phe Leu Gly Tyr Lys Ala		
	60 65 70	
gag gtg atg gtc agc cag gtg tac tca ggc agt ctg cgt gta ctc aat		293
Glu Val Met Val Ser Gln Val Tyr Ser Gly Ser Leu Arg Val Leu Asn		
	75 80 85	
cgc cac ttc tcc cag gat ctt acc cgc cgg gaa tct agt gcc ttc cgc		341
Arg His Phe Ser Gln Asp Leu Thr Arg Arg Glu Ser Ser Ala Phe Arg		
	90 95 100	
agt gaa acc gcc aaa gcc cag aag atg ctc aag gag ctc atc acc agc		389
Ser Glu Thr Ala Lys Ala Gln Lys Met Leu Lys Glu Leu Ile Thr Ser		
	105 110 115	

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acc cgc ctg gga act tac tac aac tcc agc tcc gtc tat tcc ttt ggg Thr Arg Leu Gly Thr Tyr Tyr Asn Ser Ser Ser Val Tyr Ser Phe Gly 120 125 130 135	437
gag gga ccc ctc acc tgc ttc ttc tgg ttc att ctc caa atc ccc gag Glu Gly Pro Leu Thr Cys Phe Phe Trp Phe Ile Leu Gln Ile Pro Glu 140 145 150	485
cac cgc cgg ctg atg ctg agc ccc gag gtg gtg cag gca ctg ctg gtg His Arg Arg Leu Met Leu Ser Pro Glu Val Val Gln Ala Leu Leu Val 155 160 165	533
gag gag ctg ctg tcc aca gtc aac agc tgc gct gcc gtc ccc tac agg Glu Glu Leu Leu Ser Thr Val Asn Ser Ser Ala Ala Val Pro Tyr Arg 170 175 180	581
gcc gag tac gaa gtg gac ccc gag ggc cta gtg atc ctg gaa gcc agt Ala Glu Tyr Glu Val Asp Pro Glu Gly Leu Val Ile Leu Glu Ala Ser 185 190 195	629
gtg aaa gac ata gct gca ttg aat tcc acg ctg ggt tgt tac cgc tac Val Lys Asp Ile Ala Ala Leu Asn Ser Thr Leu Gly Cys Tyr Arg Tyr 200 205 210 215	677
agc tac gtg ggc cag ggc cag gtc ctc cgg ctg aag ggg cct gac cac Ser Tyr Val Gly Gln Gly Gln Val Leu Arg Leu Lys Gly Pro Asp His 220 225 230	725
ctg gcc tcc agc tgc ctg tgg cac ctg cag ggc ccc aag gac ctc atg Leu Ala Ser Ser Cys Leu Trp His Leu Gln Gly Pro Lys Asp Leu Met 235 240 245	773
ctc aaa ctc cgg ctg gag tgg acg ctg gca gag tgc cgg gac cga ctg Leu Lys Leu Arg Leu Glu Trp Thr Leu Ala Glu Cys Arg Asp Arg Leu 250 255 260	821
gcc atg tat gac gtg gcc ggg ccc ctg gag aag agg ctc atc acc tcg Ala Met Tyr Asp Val Ala Gly Pro Leu Glu Lys Arg Leu Ile Thr Ser 265 270 275	869
gtg tac ggc tgc agc cgc cag gag ccc gtg gtg gag gtt ctg gcg tcg Val Tyr Gly Cys Ser Arg Gln Glu Pro Val Val Glu Val Leu Ala Ser 280 285 290 295	917
ggg gcc atc atg gcg gtc gtc tgg aag aag ggc ctg cac agc tac tac Gly Ala Ile Met Ala Val Val Trp Lys Lys Gly Leu His Ser Tyr Tyr 300 305 310	965
gac ccc ttc gtg ctc tcc gtg cag ccg gtg gtc ttc cag gcc tgt gaa Asp Pro Phe Val Leu Ser Val Gln Pro Val Val Phe Gln Ala Cys Glu 315 320 325	1013
gtg aac ctg acg ctg gac aac agg ctc gac tcc cag ggc gtc ctc agc Val Asn Leu Thr Leu Asp Asn Arg Leu Asp Ser Gln Gly Val Leu Ser 330 335 340	1061
acc ccg tac ttc ccc agc tac tac tcg ccc caa acc cac tgc tcc tgg Thr Pro Tyr Phe Pro Ser Tyr Tyr Ser Pro Gln Thr His Cys Ser Trp 345 350 355	1109

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cac ctc acg gtg ccc tct ctg gac tac ggc ttg gcc ctc tgg ttt gat His Leu Thr Val Pro Ser Leu Asp Tyr Gly Leu Ala Leu Trp Phe Asp 360 365 370 375	1157
gcc tat gca ctg agg agg cag aag tat gat ttg ccg tgc acc cag gcc Ala Tyr Ala Leu Arg Arg Gln Lys Tyr Asp Leu Pro Cys Thr Gln Gly 380 385 390	1205
cag tgg acg atc cag aac agg agg ctg tgt ggc ttg cgc atc ctg cag Gln Trp Thr Ile Gln Asn Arg Arg Leu Cys Gly Leu Arg Ile Leu Gln 395 400 405	1253
ccc tac gcc gag agg atc ccc gtg gtg gcc acg gcc ggg atc acc atc Pro Tyr Ala Glu Arg Ile Pro Val Val Ala Thr Ala Gly Ile Thr Ile 410 415 420	1301
aac ttc acc tcc cag atc tcc ctc acc ggg ccc ggt gtg cgg gtg cac Asn Phe Thr Ser Gln Ile Ser Leu Thr Gly Pro Gly Val Arg Val His 425 430 435	1349
tat ggc ttg tac aac cag tgc gac ccc tgc cct gga gag ttc ctc tgt Tyr Gly Leu Tyr Asn Gln Ser Asp Pro Cys Pro Gly Glu Phe Leu Cys 440 445 450 455	1397
tct gtg aat gga ctc tgt gtc cct gcc tgt gat ggg gtc aag gac tgc Ser Val Asn Gly Leu Cys Val Pro Ala Cys Asp Gly Val Lys Asp Cys 460 465 470	1445
ccc aac ggc ctg gat gag aga aac tgc gtt tgc aga gcc aca ttc cag Pro Asn Gly Leu Asp Glu Arg Asn Cys Val Cys Arg Ala Thr Phe Gln 475 480 485	1493
tgc aaa gag gac agc aca tgc atc tca ctg ccc aag gtc tgt gat ggg Cys Lys Glu Asp Ser Thr Cys Ile Ser Leu Pro Lys Val Cys Asp Gly 490 495 500	1541
cag cct gat tgt ctc aac ggc agc gac gaa gag cag tgc cag gaa ggg Gln Pro Asp Cys Leu Asn Gly Ser Asp Glu Glu Gln Cys Gln Glu Gly 505 510 515	1589
gtg cca tgt ggg aca ttc acc ttc cag tgt gag gac cgg agc tgc gtg Val Pro Cys Gly Thr Phe Thr Phe Gln Cys Glu Asp Arg Ser Cys Val 520 525 530 535	1637
aag aag ccc aac ccg cag tgt gat ggg cgg ccc gac tgc agg gac gcc Lys Lys Pro Asn Pro Gln Cys Asp Gly Arg Pro Asp Cys Arg Asp Gly 540 545 550	1685
tgc gat gag gag cac tgt gaa tgt ggc ctc cag ggc ccc tcc agc cgc Ser Asp Glu Glu His Cys Glu Cys Gly Leu Gln Gly Pro Ser Ser Arg 555 560 565	1733
att gtt ggt gga gct gtg tcc tcc gag ggt gag tgg cca tgg cag gcc Ile Val Gly Gly Ala Val Ser Ser Glu Gly Glu Trp Pro Trp Gln Ala 570 575 580	1781
agc ctc cag gtt cgg ggt cga cac atc tgt ggg ggg gcc ctc atc gct Ser Leu Gln Val Arg Gly Arg His Ile Cys Gly Gly Ala Leu Ile Ala 585 590 595	1829
gac cgc tgg gtg ata aca gct gcc cac tgc ttc cag gag gac agc atg	1877

[illegible]

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tgccctttgg aataaagctg cctgatgcaa aaaaaaaaaa aaaaaaaaaa aaa

3104

<210> 8

<211> 802

<212> PRT

<213> Homo Sapien

<400> 8

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 Asp Ser Lys Arg Lys Ala Arg Gly Tyr Leu Arg Leu Val Pro Leu Phe
 35 40 45
 Val Leu Leu Ala Leu Leu Val Leu Ala Ser Ala Gly Val Leu Leu Trp
 50 55 60
 Tyr Phe Leu Gly Tyr Lys Ala Glu Val Met Val Ser Gln Val Tyr Ser
 65 70 75 80
 Gly Ser Leu Arg Val Leu Asn Arg His Phe Ser Gln Asp Leu Thr Arg
 85 90 95
 Arg Glu Ser Ser Ala Phe Arg Ser Glu Thr Ala Lys Ala Gln Lys Met
 100 105 110
 Leu Lys Glu Leu Ile Thr Ser Thr Arg Leu Gly Thr Tyr Tyr Asn Ser
 115 120 125
 Ser Ser Val Tyr Ser Phe Gly Glu Gly Pro Leu Thr Cys Phe Phe Trp
 130 135 140
 Phe Ile Leu Gln Ile Pro Glu His Arg Arg Leu Met Leu Ser Pro Glu
 145 150 155 160
 Val Val Gln Ala Leu Leu Val Glu Glu Leu Leu Ser Thr Val Asn Ser
 165 170 175
 Ser Ala Ala Val Pro Tyr Arg Ala Glu Tyr Glu Val Asp Pro Glu Gly
 180 185 190
 Leu Val Ile Leu Glu Ala Ser Val Lys Asp Ile Ala Ala Leu Asn Ser
 195 200 205
 Thr Leu Gly Cys Tyr Arg Tyr Ser Tyr Val Gly Gln Gly Gln Val Leu
 210 215 220
 Arg Leu Lys Gly Pro Asp His Leu Ala Ser Ser Cys Leu Trp His Leu
 225 230 235 240
 Gln Gly Pro Lys Asp Leu Met Leu Lys Leu Arg Leu Glu Trp Thr Leu
 245 250 255
 Ala Glu Cys Arg Asp Arg Leu Ala Met Tyr Asp Val Ala Gly Pro Leu
 260 265 270
 Glu Lys Arg Leu Ile Thr Ser Val Tyr Gly Cys Ser Arg Gln Glu Pro
 275 280 285
 Val Val Glu Val Leu Ala Ser Gly Ala Ile Met Ala Val Val Trp Lys
 290 295 300
 Lys Gly Leu His Ser Tyr Tyr Asp Pro Phe Val Leu Ser Val Gln Pro
 305 310 315 320
 Val Val Phe Gln Ala Cys Glu Val Asn Leu Thr Leu Asp Asn Arg Leu
 325 330 335
 Asp Ser Gln Gly Val Leu Ser Thr Pro Tyr Phe Pro Ser Tyr Tyr Ser
 340 345 350
 Pro Gln Thr His Cys Ser Trp His Leu Thr Val Pro Ser Leu Asp Tyr
 355 360 365
 Gly Leu Ala Leu Trp Phe Asp Ala Tyr Ala Leu Arg Arg Gln Lys Tyr
 370 375 380
 Asp Leu Pro Cys Thr Gln Gly Gln Trp Thr Ile Gln Asn Arg Arg Leu
 385 390 395 400
 Cys Gly Leu Arg Ile Leu Gln Pro Tyr Ala Glu Arg Ile Pro Val Val
 405 410 415
 Ala Thr Ala Gly Ile Thr Ile Asn Phe Thr Ser Gln Ile Ser Leu Thr

Gly	Pro	Gly	Val	Arg	Val	His	Tyr	Gly	Leu	Tyr	Asn	Gln	Ser	Asp	Pro
		435					440					445			
Cys	Pro	Gly	Glu	Phe	Leu	Cys	Ser	Val	Asn	Gly	Leu	Cys	Val	Pro	Ala
		450				455					460				
Cys	Asp	Gly	Val	Lys	Asp	Cys	Pro	Asn	Gly	Leu	Asp	Glu	Arg	Asn	Cys
465					470					475					480
Val	Cys	Arg	Ala	Thr	Phe	Gln	Cys	Lys	Glu	Asp	Ser	Thr	Cys	Ile	Ser
				485					490					495	
Leu	Pro	Lys	Val	Cys	Asp	Gly	Gln	Pro	Asp	Cys	Leu	Asn	Gly	Ser	Asp
			500					505					510		
Glu	Glu	Gln	Cys	Gln	Glu	Gly	Val	Pro	Cys	Gly	Thr	Phe	Thr	Phe	Gln
		515					520					525			
Cys	Glu	Asp	Arg	Ser	Cys	Val	Lys	Lys	Pro	Asn	Pro	Gln	Cys	Asp	Gly
		530				535					540				
Arg	Pro	Asp	Cys	Arg	Asp	Gly	Ser	Asp	Glu	Glu	His	Cys	Glu	Cys	Gly
545					550					555					560
Leu	Gln	Gly	Pro	Ser	Ser	Arg	Ile	Val	Gly	Gly	Ala	Val	Ser	Ser	Glu
				565					570					575	
Gly	Glu	Trp	Pro	Trp	Gln	Ala	Ser	Leu	Gln	Val	Arg	Gly	Arg	His	Ile
			580					585					590		
Cys	Gly	Gly	Ala	Leu	Ile	Ala	Asp	Arg	Trp	Val	Ile	Thr	Ala	Ala	His
		595					600					605			
Cys	Phe	Gln	Glu	Asp	Ser	Met	Ala	Ser	Thr	Val	Leu	Trp	Thr	Val	Phe
		610				615					620				
Leu	Gly	Lys	Val	Trp	Gln	Asn	Ser	Arg	Trp	Pro	Gly	Glu	Val	Ser	Phe
625					630					635					640
Lys	Val	Ser	Arg	Leu	Leu	Leu	His	Pro	Tyr	His	Glu	Glu	Asp	Ser	His
				645					650					655	
Asp	Tyr	Asp	Val	Ala	Leu	Leu	Gln	Leu	Asp	His	Pro	Val	Val	Arg	Ser
			660					665					670		
Ala	Ala	Val	Arg	Pro	Val	Cys	Leu	Pro	Ala	Arg	Ser	His	Phe	Phe	Glu
		675					680					685			
Pro	Gly	Leu	His	Cys	Trp	Ile	Thr	Gly	Trp	Gly	Ala	Leu	Arg	Glu	Gly
		690				695					700				
Gly	Pro	Ile	Ser	Asn	Ala	Leu	Gln	Lys	Val	Asp	Val	Gln	Leu	Ile	Pro
705				710						715					720
Gln	Asp	Leu	Cys	Ser	Glu	Val	Tyr	Arg	Tyr	Gln	Val	Thr	Pro	Arg	Met
				725					730					735	
Leu	Cys	Ala	Gly	Tyr	Arg	Lys	Gly	Lys	Lys	Asp	Ala	Cys	Gln	Gly	Asp
			740					745					750		
Ser	Gly	Gly	Pro	Leu	Val	Cys	Lys	Ala	Leu	Ser	Gly	Arg	Trp	Phe	Leu
		755					760					765			
Ala	Gly	Leu	Val	Ser	Tr										

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<210> 9
<211> 2672
<212> DNA
<213> Homo Sapien

<220>
<221> CDS
<222> (33)...(2009)
<223> cDNA encoding: MTSP4-S (short form) splice variant

<400> 9
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	Met Pro Val Ala Glu Ala Pro	
	1 5	
cag gtg gct ggc ggg cag ggg gac gga ggt gat ggc gag gaa gcg gag	101	
Gln Val Ala Gly Gly Gln Gly Asp Gly Gly Asp Gly Glu Glu Ala Glu		
	10 15 20	
ccg gag ggg atg ttc aag gcc tgt gag gac tcc aag aga aaa gcc cgg	149	
Pro Glu Gly Met Phe Lys Ala Cys Glu Asp Ser Lys Arg Lys Ala Arg		
	25 30 35	
ggc tac ctc cgc ctg gtg ccc ctg ttt gtg ctg ctg gcc ctg ctc gtg	197	
Gly Tyr Leu Arg Leu Val Pro Leu Phe Val Leu Leu Ala Leu Leu Val		
	40 45 50 55	
ctg gct tcg ggc ggg gtg cta ctc tgg tat ttc cta ggg tac aag gcg	245	
Leu Ala Ser Ala Gly Val Leu Leu Trp Tyr Phe Leu Gly Tyr Lys Ala		
	60 65 70	
gag gtg atg gtc agc cag gtg tac tca ggc agt ctg cgt gta ctc aat	293	
Glu Val Met Val Ser Gln Val Tyr Ser Gly Ser Leu Arg Val Leu Asn		
	75 80 85	
cgc cac ttc tcc cag gat ctt acc cgc cgg gaa tct agt gcc ttc cgc	341	
Arg His Phe Ser Gln Asp Leu Thr Arg Arg Glu Ser Ser Ala Phe Arg		
	90 95 100	
agt gaa acc gcc aaa gcc cag aag atg ctc aag gag ctc atc acc agc	389	
Ser Glu Thr Ala Lys Ala Gln Lys Met Leu Lys Glu Leu Ile Thr Ser		
	105 110 115	
acc cgc ctg gga act tac tac aac tcc agc tcc gtc tat tcc ttt ggg	437	
Thr Arg Leu Gly Thr Tyr Tyr Asn Ser Ser Ser Val Tyr Ser Phe Gly		
	120 125 130 135	
gtg tac ggc tgc agc cgc cag gag ccc gtg gtg gag gtt ctg gcg tcg	485	
Val Tyr Gly Cys Ser Arg Gln Glu Pro Val Val Glu Val Leu Ala Ser		
	140 145 150	
ggg gcc atc atg gcg gtc gtc tgg aag aag ggc ctg cac agc tac tac	533	
Gly Ala Ile Met Ala Val Val Trp Lys Lys Gly Leu His Ser Tyr Tyr		
	155 160 165	
gac ccc ttc gtg ctc tcc gtg cag ccg gtg gtc ttc cag gcc tgt gaa	581	
Asp Pro Phe Val Leu Ser Val Gln Pro Val Val Phe Gln Ala Cys Glu		
	170 175 180	
gtg aac ctg acg ctg gac aac agg ctc gac tcc cag ggc gtc ctc agc	629	
Val Asn Leu Thr Leu Asp Asn Arg Leu Asp Ser Gln Gly Val Leu Ser		
	185 190 195	
acc ccg tac ttc ccc agc tac tac tcg ccc caa acc cac tgc tcc tgg	677	
Thr Pro Tyr Phe Pro Ser Tyr Tyr Ser Pro Gln Thr His Cys Ser Trp		
	200 205 210 215	
cac ctc acg gtg ccc tct ctg gac tac ggc ttg gcc ctc tgg ttt gat	725	
His Leu Thr Val Pro Ser Leu Asp Tyr Gly Leu Ala Leu Trp Phe Asp		
	220 225 230	
gcc tat gca ctg agg agg cag aag tat gat ttg ccg tgc acc cag ggc	773	

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Ala Tyr Ala Leu Arg Arg Gln Lys Tyr Asp Leu Pro Cys Thr Gln Gly	
235 240 245	
cag tgg acg atc cag aac agg agg ctg tgt ggc ttg cgc atc ctg cag	821
Gln Trp Thr Ile Gln Asn Arg Arg Leu Cys Gly Leu Arg Ile Leu Gln	
250 255 260	
ccc tac gcc gag agg atc ccc gtg gtg gcc acg gcc ggg atc acc atc	869
Pro Tyr Ala Glu Arg Ile Pro Val Val Ala Thr Ala Gly Ile Thr Ile	
265 270 275	
aac ttc acc tcc cag atc tcc ctc acc ggg ccc ggt gtg cgg gtg cac	917
Asn Phe Thr Ser Gln Ile Ser Leu Thr Gly Pro Gly Val Arg Val His	
280 285 290 295	
tat ggc ttg tac aac cag tcg gac ccc tgc cct gga gag ttc ctc tgt	965
Tyr Gly Leu Tyr Asn Gln Ser Asp Pro Cys Pro Gly Glu Phe Leu Cys	
300 305 310	
tct gtg aat gga ctc tgt gtc cct gcc tgt gat ggg gtc aag gac tgc	1013
Ser Val Asn Gly Leu Cys Val Pro Ala Cys Asp Gly Val Lys Asp Cys	
315 320 325	
ccc aac ggc ctg gat gag aga aac tgc gtt tgc aga gcc aca ttc cag	1061
Pro Asn Gly Leu Asp Glu Arg Asn Cys Val Cys Arg Ala Thr Phe Gln	
330 335 340	
tgc aaa gag gac agc aca tgc atc tca ctg ccc aag gtc tgt gat ggg	1109
Cys Lys Glu Asp Ser Thr Cys Ile Ser Leu Pro Lys Val Cys Asp Gly	
345 350 355	
cag cct gat tgt ctc aac ggc agc gac gaa gag cag tgc cag gaa ggg	1157
Gln Pro Asp Cys Leu Asn Gly Ser Asp Glu Glu Gln Cys Gln Glu Gly	
360 365 370 375	
gtg cca tgt ggg aca ttc acc ttc cag tgt gag gac cgg agc tgc gtg	1205
Val Pro Cys Gly Thr Phe Thr Phe Gln Cys Glu Asp Arg Ser Cys Val	
380 385 390	
aag aag ccc aac ccg cag tgt gat ggg cgg ccc gac tgc agg gac ggc	1253
Lys Lys Pro Asn Pro Gln Cys Asp Gly Arg Pro Asp Cys Arg Asp Gly	
395 400 405	
tcg gat gag gag cac tgt gaa tgt ggc ctc cag ggc ccc tcc agc cgc	1301
Ser Asp Glu Glu His Cys Glu Cys Gly Leu Gln Gly Pro Ser Ser Arg	
410 415 420	
att gtt ggt gga gct gtg tcc tcc gag ggt gag tgg cca tgg cag gcc	1349
Ile Val Gly Gly Ala Val Ser Ser Glu Gly Glu Trp Pro Trp Gln Ala	
425 430 435	
agc ctc cag gtt cgg ggt cga cac atc tgt ggg ggg gcc ctc atc gct	1397
Ser Leu Gln Val Arg Gly Arg His Ile Cys Gly Gly Ala Leu Ile Ala	
440 445 450 455	
gac cgc tgg gtg ata aca gct gcc cac tgc ttc cag gag gac agc atg	1445
Asp Arg Trp Val Ile Thr Ala Ala His Cys Phe Gln Glu Asp Ser Met	
460 465 470	
gcc tcc acg gtg ctg tgg acc gtg ttc ctg ggc aag gtg tgg cag aac	1493
Ala Ser Thr Val Leu Trp Thr Val Phe Leu Gly Lys Val Trp Gln Asn	

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475	480	485	
tcg cgc tgg cct gga gag gtg tcc ttc aag gtg agc cgc ctg ctc ctg			1541
Ser Arg Trp Pro Gly Glu Val Ser Phe Lys Val Ser Arg Leu Leu Leu			
490	495	500	
cac ccg tac cac gaa gag gac agc cat gac tac gac gtg gcg ctg ctg			1589
His Pro Tyr His Glu Glu Asp Ser His Asp Tyr Asp Val Ala Leu Leu			
505	510	515	
cag ctc gac cac ccg gtg gtg cgc tcg gcc gcc gtg cgc ccc gtc tgc			1637
Gln Leu Asp His Pro Val Val Arg Ser Ala Ala Val Arg Pro Val Cys			
520	525	530	535
ctg ccc gcg cgc tcc cac ttc ttc gag ccc ggc ctg cac tgc tgg att			1685
Leu Pro Ala Arg Ser His Phe Phe Glu Pro Gly Leu His Cys Trp Ile			
540	545	550	
acg ggc tgg ggc gcc ttg cgc gag ggc ggc ccc atc agc aac gct ctg			1733
Thr Gly Trp Gly Ala Leu Arg Glu Gly Gly Pro Ile Ser Asn Ala Leu			
555	560	565	
cag aaa gtg gat gtg cag ttg atc cca cag gac ctg tgc agc gag gtc			1781
Gln Lys Val Asp Val Gln Leu Ile Pro Gln Asp Leu Cys Ser Glu Val			
570	575	580	
tat cgc tac cag gtg acg cca cgc atg ctg tgt gcc ggc tac cgc aag			1829
Tyr Arg Tyr Gln Val Thr Pro Arg Met Leu Cys Ala Gly Tyr Arg Lys			
585	590	595	
ggc aag aag gat gcc tgt cag ggt gac tca ggt ggt ccg ctg gtg tgc			1877
Gly Lys Lys Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys			
600	605	610	615
aag gca ctc agt ggc cgc tgg ttc ctg gcg ggg ctg gtc agc tgg ggc			1925
Lys Ala Leu Ser Gly Arg Trp Phe Leu Ala Gly Leu Val Ser Trp Gly			
620	625	630	
ctg ggc tgt ggc cgg cct aac tac ttc ggc gtc tac acc cgc atc aca			1973
Leu Gly Cys Gly Arg Pro Asn Tyr Phe Gly Val Tyr Thr Arg Ile Thr			
635	640	645	
ggt gtg atc agc tgg atc cag caa gtg gtg acc tga ggaactgccc			2019
Gly Val Ile Ser Trp Ile Gln Gln Val Val Thr *			
650	655		
ccctgcaaag cagggccac ctccctggact cagagagccc agggcaactg ccaagcaggg			2079
ggacaagtat tctggcggg ggtgggggag agagcaggcc ctgtggtggc aggaggggca			2139
tcttggttgc tccctgatgt ctgtccagta tggcaggagg atgagaagtg ccagcagttg			2199
ggggtcaaga cgtcccttga ggacccaggc ccacaccag cccttttgcc tcccaattct			2259
ctctcctccg tccccttccct ccactgctgc ctaatgcaag gcagtggctc agcagcaaga			2319
atgctgggtc tacatccga ggagtgtctg aggtgcgccc cactctgtac agaggctgtt			2379
tgggcagcct tgcctccaga gagcagattc cagcttcgga agccccctggt ctaacttggg			2439
atctgggaat ggaaggtgct cccatcggag gggaccctca gagccctgga gactgccagg			2499
tgggcctgct gccactgtaa gccaaaaggt ggggaagtcc tgactccagg gtccttgccc			2559
cacccttgcc tgccacctgg gccctcacag ccagaccct cactgggagg tgagctcagg			2619
tgcccttttg aataaagctg cctgatgcaa aaaaaaaaaa aaaaaaaaaa aaa			2672

<210> 10
 <211> 658
 <212> PRT

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<213> Homo Sapien

<400> 10

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Met Pro Val Ala Glu Ala Pro Gln Val Ala Gly Gly Gln Gly Asp Gly
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Gly Asp Gly Glu Glu Ala Glu Pro Glu Gly Met Phe Lys Ala Cys Glu
          20          25          30
Asp Ser Lys Arg Lys Ala Arg Gly Tyr Leu Arg Leu Val Pro Leu Phe
          35          40          45
Val Leu Leu Ala Leu Leu Val Leu Ala Ser Ala Gly Val Leu Leu Trp
          50          55          60
Tyr Phe Leu Gly Tyr Lys Ala Glu Val Met Val Ser Gln Val Tyr Ser
65          70          75          80
Gly Ser Leu Arg Val Leu Asn Arg His Phe Ser Gln Asp Leu Thr Arg
          85          90          95
Arg Glu Ser Ser Ala Phe Arg Ser Glu Thr Ala Lys Ala Gln Lys Met
          100          105          110
Leu Lys Glu Leu Ile Thr Ser Thr Arg Leu Gly Thr Tyr Tyr Asn Ser
          115          120          125
Ser Ser Val Tyr Ser Phe Gly Val Tyr Gly Cys Ser Arg Gln Glu Pro
130          135          140
Val Val Glu Val Leu Ala Ser Gly Ala Ile Met Ala Val Val Trp Lys
145          150          155          160
Lys Gly Leu His Ser Tyr Tyr Asp Pro Phe Val Leu Ser Val Gln Pro
          165          170          175
Val Val Phe Gln Ala Cys Glu Val Asn Leu Thr Leu Asp Asn Arg Leu
          180          185          190
Asp Ser Gln Gly Val Leu Ser Thr Pro Tyr Phe Pro Ser Tyr Tyr Ser
          195          200          205
Pro Gln Thr His Cys Ser Trp His Leu Thr Val Pro Ser Leu Asp Tyr
210          215          220
Gly Leu Ala Leu Trp Phe Asp Ala Tyr Ala Leu Arg Arg Gln Lys Tyr
225          230          235          240
Asp Leu Pro Cys Thr Gln Gly Gln Trp Thr Ile Gln Asn Arg Arg Leu
          245          250          255
Cys Gly Leu Arg Ile Leu Gln Pro Tyr Ala Glu Arg Ile Pro Val Val
          260          265          270
Ala Thr Ala Gly Ile Thr Ile Asn Phe Thr Ser Gln Ile Ser Leu Thr
          275          280          285
Gly Pro Gly Val Arg Val His Tyr Gly Leu Tyr Asn Gln Ser Asp Pro
290          295          300
Cys Pro Gly Glu Phe Leu Cys Ser Val Asn Gly Leu Cys Val Pro Ala
305          310          315          320
Cys Asp Gly Val Lys Asp Cys Pro Asn Gly Leu Asp Glu Arg Asn Cys
          325          330          335
Val Cys Arg Ala Thr Phe Gln Cys Lys Glu Asp Ser Thr Cys Ile Ser
          340          345          350
Leu Pro Lys Val Cys Asp Gly Gln Pro Asp Cys Leu Asn Gly Ser Asp
          355          360          365
Glu Glu Gln Cys Gln Glu Gly Val Pro Cys Gly Thr Phe Thr Phe Gln
370          375          380
Cys Glu Asp Arg Ser Cys Val Lys Lys Pro Asn Pro Gln Cys Asp Gly
385          390          395          400
Arg Pro Asp Cys Arg Asp Gly Ser Asp Glu Glu His Cys Glu Cys Gly
          405          410          415
Leu Gln Gly Pro Ser Ser Arg Ile Val Gly Gly Ala Val Ser Ser Glu
          420          425          430
Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln Val Arg Gly Arg His Ile
          435          440          445
Cys Gly Gly Ala Leu Ile Ala Asp Arg Trp Val Ile Thr Ala Ala His
450          455          460

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Cys Phe Gln Glu Asp Ser Met Ala Ser Thr Val Leu Trp Thr Val Phe
 465 470 475 480
 Leu Gly Lys Val Trp Gln Asn Ser Arg Trp Pro Gly Glu Val Ser Phe
 485 490 495
 Lys Val Ser Arg Leu Leu Leu His Pro Tyr His Glu Glu Asp Ser His
 500 505 510
 Asp Tyr Asp Val Ala Leu Leu Gln Leu Asp His Pro Val Val Arg Ser
 515 520 525
 Ala Ala Val Arg Pro Val Cys Leu Pro Ala Arg Ser His Phe Phe Glu
 530 535 540
 Pro Gly Leu His Cys Trp Ile Thr Gly Trp Gly Ala Leu Arg Glu Gly
 545 550 555 560
 Gly Pro Ile Ser Asn Ala Leu Gln Lys Val Asp Val Gln Leu Ile Pro
 565 570 575
 Gln Asp Leu Cys Ser Glu Val Tyr Arg Tyr Gln Val Thr Pro Arg Met
 580 585 590
 Leu Cys Ala Gly Tyr Arg Lys Gly Lys Lys Asp Ala Cys Gln Gly Asp
 595 600 605
 Ser Gly Gly Pro Leu Val Cys Lys Ala Leu Ser Gly Arg Trp Phe Leu
 610 615 620
 Ala Gly Leu Val Ser Trp Gly Leu Gly Cys Gly Arg Pro Asn Tyr Phe
 625 630 635 640
 Gly Val Tyr Thr Arg Ile Thr Gly Val Ile Ser Trp Ile Gln Gln Val
 645 650 655
 Val Thr

<210> 11
 <211> 1656
 <212> DNA
 <213> Homo Sapien

<220>
 <221> CDS
 <222> (268)...(1629)
 <223> Nucleic acid encoding a transmembrane serine
 protease (MTSP-6) protein

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 ttgggactcg ggaattatga ctgtttttgg ttaatcgata ctgaatgcgc tttgtgtgga 120
 ctgtcgaatt tcaaagattt accgtatgac caagatgcac ctgatgctac aagtataaat 180
 aggggaacaa atgctttctg ttcttctctg gctaaggagg tagagggtga ggcggagccg 240
 gatgtcagag gtcctgaaat agtcacc atg ggg gaa aat gat ccg cct gct gtt 294
 Met Gly Glu Asn Asp Pro Pro Ala Val
 1 5
 gaa gcc ccc ttc tca ttc cga tcg ctt ttt ggc ctt gat gat ttg aaa 342
 Glu Ala Pro Phe Ser Phe Arg Ser Leu Phe Gly Leu Asp Asp Leu Lys
 10 15 20 25
 ata agt cct gtt gca cca gat gca gat gct gtt gct gca cag atc ctg 390
 Ile Ser Pro Val Ala Pro Asp Ala Asp Ala Val Ala Ala Gln Ile Leu
 30 35 40
 tca ctg ctg cca ttg aag ttt ttt cca atc atc gtc att ggg atc att 438
 Ser Leu Leu Pro Leu Lys Phe Phe Pro Ile Ile Val Ile Gly Ile Ile
 45 50 55
 gca ttg ata tta gca ctg gcc att ggt ctg ggc atc cac ttc gac tgc 486
 Ala Leu Ile Leu Ala Leu Ala Ile Gly Leu Gly Ile His Phe Asp Cys

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60	65	70	
tca ggg aag tac aga tgt cgc tca tcc ttt aag tgt atc gag ctg ata Ser Gly Lys Tyr Arg Cys Arg Ser Ser Phe Lys Cys Ile Glu Leu Ile 75 80 85			534
gct cga tgt gac gga gtc tcg gat tgc aaa gac ggg gag gac gag tac Ala Arg Cys Asp Gly Val Ser Asp Cys Lys Asp Gly Glu Asp Glu Tyr 90 95 100 105			582
cgc tgt gtc cgg gtg ggt ggt cag aat gcc gtg ctc cag gtg ttc aca Arg Cys Val Arg Val Gly Gly Gln Asn Ala Val Leu Gln Val Phe Thr 110 115 120			630
gct gct tcg tgg aag acc atg tgc tcc gat gac tgg aag ggt cac tac Ala Ala Ser Trp Lys Thr Met Cys Ser Asp Asp Trp Lys Gly His Tyr 125 130 135			678
gca aat gtt gcc tgt gcc caa ctg ggt ttc cca agc tat gta agt tca Ala Asn Val Ala Cys Ala Gln Leu Gly Phe Pro Ser Tyr Val Ser Ser 140 145 150			726
gat aac ctc aga gtg agc tcg cta gag ggg cag ttc cgg gag gag ttt Asp Asn Leu Arg Val Ser Ser Leu Glu Gly Gln Phe Arg Glu Glu Phe 155 160 165			774
gtg tcc atc gat cac ctc ttg cca gat gac aag gtg act gca tta cac Val Ser Ile Asp His Leu Leu Pro Asp Asp Lys Val Thr Ala Leu His 170 175 180 185			822
cac tca gta tat gtg agg gag gga tgt gcc tct ggc cac gtg gtt acc His Ser Val Tyr Val Arg Glu Gly Cys Ala Ser Gly His Val Val Thr 190 195 200			870
ttg cag tgc aca gcc tgt ggt cat aga agg ggc tac agc tca cgc atc Leu Gln Cys Thr Ala Cys Gly His Arg Arg Gly Tyr Ser Ser Arg Ile 205 210 215			918
gtg ggt gga aac atg tcc ttg ctc tcg cag tgg ccc tgg cag gcc agc Val Gly Gly Asn Met Ser Leu Leu Ser Gln Trp Pro Trp Gln Ala Ser 220 225 230			966
ctt cag ttc cag ggc tac cac ctg tgc ggg ggc tct gtc atc acg ccc Leu Gln Phe Gln Gly Tyr His Leu Cys Gly Gly Ser Val Ile Thr Pro 235 240 245			1014
ctg tgg atc atc act gct gca cac tgt gtt tat gac ttg tac ctc ccc Leu Trp Ile Ile Thr Ala Ala His Cys Val Tyr Asp Leu Tyr Leu Pro 250 255 260 265			1062
aag tca tgg acc atc cag gtg ggt cta gtt tcc ctg ttg gac aat cca Lys Ser Trp Thr Ile Gln Val Gly Leu Val Ser Leu Leu Asp Asn Pro 270 275 280			1110
gcc cca tcc cac ttg gtg gag aag att gtc tac cac agc aag tac aag Ala Pro Ser His Leu Val Glu Lys Ile Val Tyr His Ser Lys Tyr Lys 285 290 295			1158
cca aag agg ctg ggc aat gac atc gcc ctt atg aag ctg gcc ggg cca Pro Lys Arg Leu Gly Asn Asp Ile Ala Leu Met Lys Leu Ala Gly Pro 300 305 310			1206

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ctc acg ttc aat gaa atg atc cag cct gtg tgc ctg ccc aac tct gaa 1254
 Leu Thr Phe Asn Glu Met Ile Gln Pro Val Cys Leu Pro Asn Ser Glu
 315 320 325

gag aac ttc ccc gat gga aaa gtg tgc tgg acg tca gga tgg ggg gcc 1302
 Glu Asn Phe Pro Asp Gly Lys Val Cys Trp Thr Ser Gly Trp Gly Ala
 330 335 340 345

aca gag gat gga ggt gac gcc tcc cct gtc ctg aac cac gcg gcc gtc 1350
 Thr Glu Asp Gly Gly Asp Ala Ser Pro Val Leu Asn His Ala Ala Val
 350 355 360

cct ttg att tcc aac aag atc tgc aac cac agg gac gtg tac ggt ggc 1398
 Pro Leu Ile Ser Asn Lys Ile Cys Asn His Arg Asp Val Tyr Gly Gly
 365 370 375

atc atc tcc ccc tcc atg ctc tgc gcg ggc tac ctg acg ggt ggc gtg 1446
 Ile Ile Ser Pro Ser Met Leu Cys Ala Gly Tyr Leu Thr Gly Gly Val
 380 385 390

gac agc tgc cag ggg gac agc ggg ggg ccc ctg gtg tgt caa gag agg 1494
 Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gln Glu Arg
 395 400 405

agg ctg tgg aag tta gtg gga gcg acc agc ttt ggc atc ggc tgc gca 1542
 Arg Leu Trp Lys Leu Val Gly Ala Thr Ser Phe Gly Ile Gly Cys Ala
 410 415 420 425

gag gtg aac aag cct ggg gtg tac acc cgt gtc acc tcc ttc ctg gac 1590
 Glu Val Asn Lys Pro Gly Val Tyr Thr Arg Val Thr Ser Phe Leu Asp
 430 435 440

tgg atc cac gag cag atg gag aga gac cta aaa acc tga agaggaaggg 1639
 Trp Ile His Glu Gln Met Glu Arg Asp Leu Lys Thr *
 445 450

gataagtagc cacctga 1656

<210> 12
 <211> 453
 <212> PRT
 <213> Homo Sapien

<400> 12
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 1 5 10 15
 Ser Leu Phe Gly Leu Asp Asp Leu Lys Ile Ser Pro Val Ala Pro Asp
 20 25 30
 Ala Asp Ala Val Ala Ala Gln Ile Leu Ser Leu Leu Pro Leu Lys Phe
 35 40 45
 Phe Pro Ile Ile Val Ile Gly Ile Ile Ala Leu Ile Leu Ala Leu Ala
 50 55 60
 Ile Gly Leu Gly Ile His Phe Asp Cys Ser Gly Lys Tyr Arg Cys Arg
 65 70 75 80
 Ser Ser Phe Lys Cys Ile Glu Leu Ile Ala Arg Cys Asp Gly Val Ser
 85 90 95
 Asp Cys Lys Asp Gly Glu Asp Glu Tyr Arg Cys Val Arg Val Gly Gly
 100 105 110
 Gln Asn Ala Val Leu Gln Val Phe Thr Ala Ala Ser Trp Lys Thr Met
 115 120 125

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Cys Ser Asp Asp Trp Lys Gly His Tyr Ala Asn Val Ala Cys Ala Gln
 130 135 140
 Leu Gly Phe Pro Ser Tyr Val Ser Ser Asp Asn Leu Arg Val Ser Ser
 145 150 155 160
 Leu Glu Gly Gln Phe Arg Glu Glu Phe Val Ser Ile Asp His Leu Leu
 165 170 175
 Pro Asp Asp Lys Val Thr Ala Leu His His Ser Val Tyr Val Arg Glu
 180 185 190
 Gly Cys Ala Ser Gly His Val Val Thr Leu Gln Cys Thr Ala Cys Gly
 195 200 205
 His Arg Arg Gly Tyr Ser Ser Arg Ile Val Gly Gly Asn Met Ser Leu
 210 215 220
 Leu Ser Gln Trp Pro Trp Gln Ala Ser Leu Gln Phe Gln Gly Tyr His
 225 230 235 240
 Leu Cys Gly Gly Ser Val Ile Thr Pro Leu Trp Ile Ile Thr Ala Ala
 245 250 255
 His Cys Val Tyr Asp Leu Tyr Leu Pro Lys Ser Trp Thr Ile Gln Val
 260 265 270
 Gly Leu Val Ser Leu Leu Asp Asn Pro Ala Pro Ser His Leu Val Glu
 275 280 285
 Lys Ile Val Tyr His Ser Lys Tyr Lys Pro Lys Arg Leu Gly Asn Asp
 290 295 300
 Ile Ala Leu Met Lys Leu Ala Gly Pro Leu Thr Phe Asn Glu Met Ile
 305 310 315 320
 Gln Pro Val Cys Leu Pro Asn Ser Glu Glu Asn Phe Pro Asp Gly Lys
 325 330 335
 Val Cys Trp Thr Ser Gly Trp Gly Ala Thr Glu Asp Gly Gly Asp Ala
 340 345 350
 Ser Pro Val Leu Asn His Ala Ala Val Pro Leu Ile Ser Asn Lys Ile
 355 360 365
 Cys Asn His Arg Asp Val Tyr Gly Gly Ile Ile Ser Pro Ser Met Leu
 370 375 380
 Cys Ala Gly Tyr Leu Thr Gly Gly Val Asp Ser Cys Gln Gly Asp Ser
 385 390 395 400
 Gly Gly Pro Leu Val Cys Gln Glu Arg Arg Leu Trp Lys Leu Val Gly
 405 410 415
 Ala Thr Ser Phe Gly Ile Gly Cys Ala Glu Val Asn Lys Pro Gly Val
 420 425 430
 Tyr Thr Arg Val Thr Ser Phe Leu Asp Trp Ile His Glu Gln Met Glu
 435 440 445
 Arg Asp Leu Lys Thr
 450

<210> 13

<211> 2100

<212> DNA

<213> Homo sapien

<220>

<221> CDS

<222> (45)...(1361)

<223> Nucleic acid encoding MTSP7

<400> 13

agatcagatg gcgactgaat agaagctgcc ccagtcctgg gttc atg atg tac aca
 Met Met Tyr Thr
 1

56

cct gtt gaa ttt tca gaa gct gaa ttc tca cga gct gaa tat caa aga
 Pro Val Glu Phe Ser Glu Ala Glu Phe Ser Arg Ala Glu Tyr Gln Arg
 5 10 15 20

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aag cag caa ttt tgg gac tca gta cgg cta gct ctt ttc aca tta gca	152
Lys Gln Gln Phe 25	Leu Ala Leu Phe Thr Leu Ala 30 35
att gta gca atc ata gga att gca att ggt att gtt act cat ttt gtt	200
Ile Val Ala 40	Ile Gly Ile Ala 45
ggt gag gat gat aag tct ttc tat tac ctt gcc tct ttt aaa gtc aca	248
Val Glu Asp 55	Lys Ser Phe Tyr Tyr Leu Ala Ser Phe Lys Val Thr 60 65
aat atc aaa tat aaa gaa aat tat ggc ata aga tct tca aga gag ttt	296
Asn Ile Lys Tyr Lys Glu Asn Tyr Gly Ile Arg Ser Ser Arg Glu Phe	70 75 80
ata gaa agg agt cat cag att gaa aga atg atg tct agg ata ttt cga	344
Ile Glu Arg Ser His Gln Ile Glu Arg Met Met Ser Arg Ile Phe Arg	85 90 95 100
cat tct tct gta ggc ggt cga ttt atc aaa tct cat gtt atc aaa tta	392
His Ser Ser Val Gly Gly Arg Phe Ile Lys Ser His Val Ile Lys Leu	105 110 115
agt cca gat gaa caa ggt gtg gat att ctt ata gtg ctc ata ttt cga	440
Ser Pro Asp Glu Gln Gly Val Asp Ile Leu Ile Val Leu Ile Phe Arg	120 125 130
tac cca tct act gat agt gct gaa caa atc aag aaa aaa att gaa aag	488
Tyr Pro Ser Thr Asp Ser Ala Glu Gln Ile Lys Lys Lys Ile Glu Lys	135 140 145
gct tta tat caa agt ttg aag acc aaa caa ttg tct ttg acc ata aac	536
Ala Leu Tyr Gln Ser Leu Lys Thr Lys Gln Leu Ser Leu Thr Ile Asn	150 155 160
aaa cca tca ttt aga ctc aca cct att gac agc aaa aag atg agg aat	584
Lys Pro Ser Phe Arg Leu Thr Pro Ile Asp Ser Lys Lys Met Arg Asn	165 170 175 180
ctt ctc aac agt cgc tgt gga ata agg atg aca tct tca aac atg cca	632
Leu Leu Asn Ser Arg Cys Gly Ile Arg Met Thr Ser Ser Asn Met Pro	185 190 195
tta cca gca tcc tct tct act caa aga att gtc caa gga agg gaa aca	680
Leu Pro Ala Ser Ser Ser Thr Gln Arg Ile Val Gln Gly Arg Glu Thr	200 205 210
gct atg gaa ggg gaa tgg cca tgg cag gcc agc ctc cag ctc ata ggg	728
Ala Met Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln Leu Ile Gly	215 220 225
tca ggc cat cag tgt gga gcc agc ctc atc agt aac aca tgg ctg ctc	776
Ser Gly His Gln Cys Gly Ala Ser Leu Ile Ser Asn Thr Trp Leu Leu	230 235 240
aca gca gct cac tgc ttt tgg aaa aat aaa gac cca act caa tgg att	824
Thr Ala Ala His Cys Phe Trp Lys Asn Lys Asp Pro Thr Gln Trp Ile	245 250 255 260

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gct act ttt ggt gca act ata aca cca ccc gca gtg aaa cga aat gtg Ala Thr Phe Gly Ala Thr Ile Thr Pro Pro Ala Val Lys Arg Asn Val 265 270 275	872
agg aaa att att ctt cat gag aat tac cat aga gaa aca aat gaa aat Arg Lys Ile Ile Leu His Glu Asn Tyr His Arg Glu Thr Asn Glu Asn 280 285 290	920
gac att gct ttg gtt cag ctc tct act gga gtt gag ttt tca aat ata Asp Ile Ala Leu Val Gln Leu Ser Thr Gly Val Glu Phe Ser Asn Ile 295 300 305	968
gtc cag aga gtt tgc ctc cca gac tca tct ata aag ttg cca cct aaa Val Gln Arg Val Cys Leu Pro Asp Ser Ser Ile Lys Leu Pro Pro Lys 310 315 320	1016
aca agt gtg ttc gtc aca gga ttt gga tcc att gta gat gat gga cct Thr Ser Val Phe Val Thr Gly Phe Gly Ser Ile Val Asp Asp Gly Pro 325 330 335 340	1064
ata caa aat aca ctt cgg caa gcc aga gtg gaa acc ata agc act gat Ile Gln Asn Thr Leu Arg Gln Ala Arg Val Glu Thr Ile Ser Thr Asp 345 350 355	1112
gtg tgt aac aga aag gat gtg tat gat ggc ctg ata act cca gga atg Val Cys Asn Arg Lys Asp Val Tyr Asp Gly Leu Ile Thr Pro Gly Met 360 365 370	1160
tta tgt gct gga ttc atg gaa gga aaa ata gat gca tgt aag gga gat Leu Cys Ala Gly Phe Met Glu Gly Lys Ile Asp Ala Cys Lys Gly Asp 375 380 385	1208
tct ggt gga cct ctg gtt tat gat aat cat gac atc tgg tac att gta Ser Gly Gly Pro Leu Val Tyr Asp Asn His Asp Ile Trp Tyr Ile Val 390 395 400	1256
ggt ata gta agt tgg gga caa tca tgt gca ctt ccc aaa aaa cct gga Gly Ile Val Ser Trp Gly Gln Ser Cys Ala Leu Pro Lys Lys Pro Gly 405 410 415 420	1304
gtc tac acc aga gta act aag tat cga gat tgg att gcc tca aag act Val Tyr Thr Arg Val Thr Lys Tyr Arg Asp Trp Ile Ala Ser Lys Thr 425 430 435	1352
ggt atg tag tgtggattgt ccatgagtta tacacatggc acacagagct Gly Met *	1401
gatactcctg cgtatTTTTgt attgtttaa ttcattttact ttggattagt gcttttgcta gatgtcaaga agcccttcag acccagacaa atctaatac ctgaggtggc ctttacatac gtaggaccaa accctctcta ccatgagggg agaagacaca gcaaatgaca gacagcacct attccttact cacaagggaa actgcttggtg atacttccta ataagataaa taagtgggtt ccctcaattg aagacaggaa catcattttc cacaggatat gaagagctgc cagtaatgcc aaaatcttac ctcatataat acctggagca tgtgagattc ttctagttaa aaagaacagt cttccctgaa gactcagggc ttcaacattc tagaactgat aagtggacct tcagtgtgca agaatggaga agcatgggat ttgcattatg acttgaactg ggcttatatc taataatata gagcactatc actaacctca acagttgaca ttttaaaagt ttttaaatgt atctgaactt gctgttaaca cagtgttata actcaagcac tagcttcagg aagcatgttg tgttggttaag aagcttttct gattttattct ttaacagcat cttgccatct atatgttagt agcagttggc ccagaaagga caaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	1461 1521 1581 1641 1701 1761 1821 1881 1941 2001 2061 2100

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<210> 14
 <211> 438
 <212> PRT
 <213> Homo sapien

<400> 14
 Met Met Tyr Thr Pro Val Glu Phe Ser Glu Ala Glu Phe Ser Arg Ala
 1 5 10 15
 Glu Tyr Gln Arg Lys Gln Gln Phe Trp Asp Ser Val Arg Leu Ala Leu
 20 25 30
 Phe Thr Leu Ala Ile Val Ala Ile Ile Gly Ile Ala Ile Gly Ile Val
 35 40 45
 Thr His Phe Val Val Glu Asp Lys Ser Phe Tyr Tyr Leu Ala Ser
 50 55 60
 Phe Lys Val Thr Asn Ile Lys Tyr Lys Glu Asn Tyr Gly Ile Arg Ser
 65 70 75 80
 Ser Arg Glu Phe Ile Glu Arg Ser His Gln Ile Glu Arg Met Met Ser
 85 90 95
 Arg Ile Phe Arg His Ser Ser Val Gly Gly Arg Phe Ile Lys Ser His
 100 105 110
 Val Ile Lys Leu Ser Pro Asp Glu Gln Gly Val Asp Ile Leu Ile Val
 115 120 125
 Leu Ile Phe Arg Tyr Pro Ser Thr Asp Ser Ala Glu Gln Ile Lys Lys
 130 135 140
 Lys Ile Glu Lys Ala Leu Tyr Gln Ser Leu Lys Thr Lys Gln Leu Ser
 145 150 155 160
 Leu Thr Ile Asn Lys Pro Ser Phe Arg Leu Thr Pro Ile Asp Ser Lys
 165 170 175
 Lys Met Arg Asn Leu Leu Asn Ser Arg Cys Gly Ile Arg Met Thr Ser
 180 185 190
 Ser Asn Met Pro Leu Pro Ala Ser Ser Ser Thr Gln Arg Ile Val Gln
 195 200 205
 Gly Arg Glu Thr Ala Met Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu
 210 215 220
 Gln Leu Ile Gly Ser Gly His Gln Cys Gly Ala Ser Leu Ile Ser Asn
 225 230 235 240
 Thr Trp Leu Leu Thr Ala Ala His Cys Phe Trp Lys Asn Lys Asp Pro
 245 250 255
 Thr Gln Trp Ile Ala Thr Phe Gly Ala Thr Ile Thr Pro Pro Ala Val
 260 265 270
 Lys Arg Asn Val Arg Lys Ile Ile Leu His Glu Asn Tyr His Arg Glu
 275 280 285
 Thr Asn Glu Asn Asp Ile Ala Leu Val Gln Leu Ser Thr Gly Val Glu
 290 295 300
 Phe Ser Asn Ile Val Gln Arg Val Cys Leu Pro Asp Ser Ser Ile Lys
 305 310 315 320
 Leu Pro Pro Lys Thr Ser Val Phe Val Thr Gly Phe Gly Ser Ile Val
 325 330 335
 Asp Asp Gly Pro Ile Gln Asn Thr Leu Arg Gln Ala Arg Val Glu Thr
 340 345 350
 Ile Ser Thr Asp Val Cys Asn Arg Lys Asp Val Tyr Asp Gly Leu Ile
 355 360 365
 Thr Pro Gly Met Leu Cys Ala Gly Phe Met Glu Gly Lys Ile Asp Ala
 370 375 380
 Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Tyr Asp Asn His Asp Ile
 385 390 395 400
 Trp Tyr Ile Val Gly Ile Val Ser Trp Gly Gln Ser Cys Ala Leu Pro
 405 410 415
 Lys Lys Pro Gly Val Tyr Thr Arg Val Thr Lys Tyr Arg Asp Trp Ile
 420 425 430
 Ala Ser Lys Thr Gly Met

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435

<210> 15
 <211> 702
 <212> DNA
 <213> Homo sapien

<220>
 <221> CDS
 <222> (1)...(702)
 <223> Nucleotide sequence encoding MTSP-7 Protease Domain

<400> 15
 att gtc caa gga agg gaa aca gct atg gaa ggg gaa tgg cca tgg cag 48
 Ile Val Gln Gly Arg Glu Thr Ala Met Glu Gly Glu Trp Pro Trp Gln
 1 5 10 15

gcc agc ctc cag ctc ata ggg tca ggc cat cag tgt gga gcc agc ctc 96
 Ala Ser Leu Gln Leu Ile Gly Ser Gly His Gln Cys Gly Ala Ser Leu
 20 25 30

atc agt aac aca tgg ctg ctc aca gca gct cac tgc ttt tgg aaa aat 144
 Ile Ser Asn Thr Trp Leu Leu Thr Ala Ala His Cys Phe Trp Lys Asn
 35 40 45

aaa gac cca act caa tgg att gct act ttt ggt gca act ata aca cca 192
 Lys Asp Pro Thr Gln Trp Ile Ala Thr Phe Gly Ala Thr Ile Thr Pro
 50 55 60

ccc gca gtg aaa cga aat gtg agg aaa att att ctt cat gag aat tac 240
 Pro Ala Val Lys Arg Asn Val Arg Lys Ile Ile Leu His Glu Asn Tyr
 65 70 75 80

cat aga gaa aca aat gaa aat gac att gct ttg gtt cag ctc tct act 288
 His Arg Glu Thr Asn Glu Asn Asp Ile Ala Leu Val Gln Leu Ser Thr
 85 90 95

gga gtt gag ttt tca aat ata gtc cag aga gtt tgc ctc cca gac tca 336
 Gly Val Glu Phe Ser Asn Ile Val Gln Arg Val Cys Leu Pro Asp Ser
 100 105 110

tct ata aag ttg cca cct aaa aca agt gtg ttc gtc aca gga ttt gga 384
 Ser Ile Lys Leu Pro Pro Lys Thr Ser Val Phe Val Thr Gly Phe Gly
 115 120 125

tcc att gta gat gat gga cct ata caa aat aca ctt cgg caa gcc aga 432
 Ser Ile Val Asp Asp Gly Pro Ile Gln Asn Thr Leu Arg Gln Ala Arg
 130 135 140

gtg gaa acc ata agc act gat gtg tgt aac aga aag gat gtg tat gat 480
 Val Glu Thr Ile Ser Thr Asp Val Cys Asn Arg Lys Asp Val Tyr Asp
 145 150 155 160

ggc ctg ata act cca gga atg tta tgt gct gga ttc atg gaa gga aaa 528
 Gly Leu Ile Thr Pro Gly Met Leu Cys Ala Gly Phe Met Glu Gly Lys
 165 170 175

ata gat gca tgt aag gga gat tct ggt gga cct ctg gtt tat gat aat 576
 Ile Asp Ala Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Tyr Asp Asn
 180 185 190

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cat gac atc tgg tac att gta ggt ata gta agt tgg gga caa tca tgt      624
His Asp Ile Trp Tyr Ile Val Gly Ile Val Ser Trp Gly Gln Ser Cys
      195                200                205

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gca ctt ccc aaa aaa cct gga gtc tac acc aga gta act aag tat cga      672
Ala Leu Pro Lys Lys Pro Gly Val Tyr Thr Arg Val Thr Lys Tyr Arg
      210                215                220

```

```

gat tgg att gcc tca aag act ggt atg tag      702
Asp Trp Ile Ala Ser Lys Thr Gly Met *
      225                230

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<210> 16
<211> 233
<212> PRT
<213> Homo sapien

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<400> 16
Ile Val Gln Gly Arg Glu Thr Ala Met Glu Gly Glu Trp Pro Trp Gln
  1      5      10      15
Ala Ser Leu Gln Leu Ile Gly Ser Gly His Gln Cys Gly Ala Ser Leu
      20      25      30
Ile Ser Asn Thr Trp Leu Leu Thr Ala Ala His Cys Phe Trp Lys Asn
      35      40      45
Lys Asp Pro Thr Gln Trp Ile Ala Thr Phe Gly Ala Thr Ile Thr Pro
      50      55      60
Pro Ala Val Lys Arg Asn Val Arg Lys Ile Ile Leu His Glu Asn Tyr
      65      70      75      80
His Arg Glu Thr Asn Glu Asn Asp Ile Ala Leu Val Gln Leu Ser Thr
      85      90      95
Gly Val Glu Phe Ser Asn Ile Val Gln Arg Val Cys Leu Pro Asp Ser
      100     105     110
Ser Ile Lys Leu Pro Pro Lys Thr Ser Val Phe Val Thr Gly Phe Gly
      115     120     125
Ser Ile Val Asp Asp Gly Pro Ile Gln Asn Thr Leu Arg Gln Ala Arg
      130     135     140
Val Glu Thr Ile Ser Thr Asp Val Cys Asn Arg Lys Asp Val Tyr Asp
      145     150     155     160
Gly Leu Ile Thr Pro Gly Met Leu Cys Ala Gly Phe Met Glu Gly Lys
      165     170     175
Ile Asp Ala Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Tyr Asp Asn
      180     185     190
His Asp Ile Trp Tyr Ile Val Gly Ile Val Ser Trp Gly Gln Ser Cys
      195     200     205
Ala Leu Pro Lys Lys Pro Gly Val Tyr Thr Arg Val Thr Lys Tyr Arg
      210     215     220
Asp Trp Ile Ala Ser Lys Thr Gly Met
      225     230

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<210> 17
<211> 777
<212> DNA
<213> Homo Sapien

```

```

<220>
<221> CDS
<222> (1)...(729)
<223> Nucleotide sequence encoding MTSP9, including
      protease domain (31-729)

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<400> 17
 aaa cga gtt gtt cca tta aac gtc aac aga ata gca tct gga gtc att 48
 Lys Arg Val Val Pro Leu Asn Val Asn Arg Ile Ala Ser Gly Val Ile
 1 5 10 15

gca ccc aag gcg gcc tgg cct tgg caa gct tcc ctt cag tat gat aac 96
 Ala Pro Lys Ala Ala Trp Pro Trp Gln Ala Ser Leu Gln Tyr Asp Asn
 20 25 30

atc cat cag tgt ggg gcc acc ttg att agt aac aca tgg ctt gtc act 144
 Ile His Gln Cys Gly Ala Thr Leu Ile Ser Asn Thr Trp Leu Val Thr
 35 40 45

gca gca cac tgc ttc cag aag tat aaa aat cca cat caa tgg act gtt 192
 Ala Ala His Cys Phe Gln Lys Tyr Lys Asn Pro His Gln Trp Thr Val
 50 55 60

agt ttt gga aca aaa atc aac cct ccc tta atg aaa aga aat gtc aga 240
 Ser Phe Gly Thr Lys Ile Asn Pro Pro Leu Met Lys Arg Asn Val Arg
 65 70 75 80

aga ttt att atc cat gag aag tac cgc tct gca gca aga gag tac gac 288
 Arg Phe Ile Ile His Glu Lys Tyr Arg Ser Ala Ala Arg Glu Tyr Asp
 85 90 95

att gct gtt gtg cag gtc tct tcc aga gtc acc ttt tgg gat gac ata 336
 Ile Ala Val Val Gln Val Ser Ser Arg Val Thr Phe Ser Asp Asp Ile
 100 105 110

cgc cgg att tgt ttg cca gaa gcc tct gca tcc ttc caa cca aat ttg 384
 Arg Arg Ile Cys Leu Pro Glu Ala Ser Ala Ser Phe Gln Pro Asn Leu
 115 120 125

act gtc cac atc aca gga ttt gga gca ctt tac tat ggt ggg gaa tcc 432
 Thr Val His Ile Thr Gly Phe Gly Ala Leu Tyr Tyr Gly Gly Glu Ser
 130 135 140

caa aat gat ctc cga gaa gcc aga gtg aaa atc ata agt gac gat gtc 480
 Gln Asn Asp Leu Arg Glu Ala Arg Val Lys Ile Ile Ser Asp Asp Val
 145 150 155 160

tgc aag caa cca cag gtg tat ggc aat gat ata aaa cct gga atg ttc 528
 Cys Lys Gln Pro Gln Val Tyr Gly Asn Asp Ile Lys Pro Gly Met Phe
 165 170 175

tgt gcc gga tat atg gaa gga att tat gat gcc tgc agg ggt gat tct 576
 Cys Ala Gly Tyr Met Glu Gly Ile Tyr Asp Ala Cys Arg Gly Asp Ser
 180 185 190

ggg gga cct tta gtc aca agg gat ctg aaa gat acg tgg tat ctc att 624
 Gly Gly Pro Leu Val Thr Arg Asp Leu Lys Asp Thr Trp Tyr Leu Ile
 195 200 205

gga att gta agc tgg gga gat aac tgt ggt caa aag gac aag cct gga 672
 Gly Ile Val Ser Trp Gly Asp Asn Cys Gly Gln Lys Asp Lys Pro Gly
 210 215 220

gtc tac aca caa gtg act tat tac cga aac tgg att gct tca aaa aca 720
 Val Tyr Thr Gln Val Thr Tyr Tyr Arg Asn Trp Ile Ala Ser Lys Thr
 225 230 235 240

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ggc atc taa ttcacgataa aagttaaaca aagaaagctg tatgcaggtc atatatgc 777
Gly Ile

<210> 18

<211> 242

<212> PRT

<213> Homo Sapien

<220>

<221> SITE

<222> (11)...(242)

<223> MTSP9 protease domain

<400> 18

Lys Arg Val Val Pro Leu Asn Val Asn Arg Ile Ala Ser Gly Val Ile
1 5 10 15

Ala Pro Lys Ala Ala Trp Pro Trp Gln Ala Ser Leu Gln Tyr Asp Asn
20 25 30

Ile His Gln Cys Gly Ala Thr Leu Ile Ser Asn Thr Trp Leu Val Thr
35 40 45

Ala Ala His Cys Phe Gln Lys Tyr Lys Asn Pro His Gln Trp Thr Val
50 55 60

Ser Phe Gly Thr Lys Ile Asn Pro Pro Leu Met Lys Arg Asn Val Arg
65 70 75 80

Arg Phe Ile Ile His Glu Lys Tyr Arg Ser Ala Ala Arg Glu Tyr Asp
85 90 95

Ile Ala Val Val Gln Val Ser Ser Arg Val Thr Phe Ser Asp Asp Ile
100 105 110

Arg Arg Ile Cys Leu Pro Glu Ala Ser Ala Ser Phe Gln Pro Asn Leu
115 120 125

Thr Val His Ile Thr Gly Phe Gly Ala Leu Tyr Tyr Gly Gly Glu Ser
130 135 140

Gln Asn Asp Leu Arg Glu Ala Arg Val Lys Ile Ile Ser Asp Asp Val
145 150 155 160

Cys Lys Gln Pro Gln Val Tyr Gly Asn Asp Ile Lys Pro Gly Met Phe
165 170 175

Cys Ala Gly Tyr Met Glu Gly Ile Tyr Asp Ala Cys Arg Gly Asp Ser
180 185 190

Gly Gly Pro Leu Val Thr Arg Asp Leu Lys Asp Thr Trp Tyr Leu Ile
195 200 205

Gly Ile Val Ser Trp Gly Asp Asn Cys Gly Gln Lys Asp Lys Pro Gly
210 215 220

Val Tyr Thr Gln Val Thr Tyr Tyr Arg Asn Trp Ile Ala Ser Lys Thr
225 230 235 240

Gly Ile

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<210> 19 MTSP12
 <211> 3316
 <212> DNA
 <213> Homo Sapien

<220>
 <221> CDS
 <222> (1)...(3282)
 <223> Nucleotide sequence encoding MTSP12, including
 MTSP12-PD1, MTSP12-PD2, and MTSP12-PD3 protease
 domains

<400> 19
 atg gag ccc act gtg gct aac gta cac ctc gtg ccc agg aca acc aag 48
 Met Glu Pro Thr Val Ala Asn Val His Leu Val Pro Arg Thr Thr Lys
 1 5 10 15
 gaa gtc ccc gct ctg gat gcc gcg tgc tgt cga gcg gcc acc att ggc 96
 Glu Val Pro Ala Leu Asp Ala Ala Cys Cys Arg Ala Ala Thr Ile Gly
 20 25 30
 gtg gtg gcc acc agc ctt gtc gtc ctc acc ctg gga gtc ctt ttg gcc 144
 Val Val Ala Thr Ser Leu Val Val Leu Thr Leu Gly Val Leu Leu Ala
 35 40 45
 ttc ctc tct aca cag ggc ttc cac gtg gac cac acg gcc gag ctg cgg 192
 Phe Leu Ser Thr Gln Gly Phe His Val Asp His Thr Ala Glu Leu Arg
 50 55 60
 gga atc cgg tgg acc agc agt ttg cgg cgg gag acc tcg gac tat cac 240
 Gly Ile Arg Trp Thr Ser Ser Leu Arg Arg Glu Thr Ser Asp Tyr His
 65 70 75 80
 cgc acg ctg acg ccc acc ctg gag gca ctg ttt gta agt agt ttt cag 288
 Arg Thr Leu Thr Pro Thr Leu Glu Ala Leu Phe Val Ser Ser Phe Gln
 85 90 95
 aag aca gag tta gag gca agc tgc gtg ggt tgc tcg gta ctg aat tat 336
 Lys Thr Glu Leu Glu Ala Ser Cys Val Gly Cys Ser Val Leu Asn Tyr
 100 105 110
 agg gat ggg aac tcc agt gtc ctc gta cat ttc cag ctg cac ttt ctg 384
 Arg Asp Gly Asn Ser Ser Val Leu Val His Phe Gln Leu His Phe Leu
 115 120 125
 ctg cga ccc ctc cag acg ctg agc ctg ggc ctg gag gag gag cta ttg 432
 Leu Arg Pro Leu Gln Thr Leu Ser Leu Gly Leu Glu Glu Glu Leu Leu
 130 135 140
 cag cga ggg atc cgg gca agg ctg cgg gag cac ggc atc tcc ctg gct 480
 Gln Arg Gly Ile Arg Ala Arg Leu Arg Glu His Gly Ile Ser Leu Ala
 145 150 155 160
 gcc tat gcc aca att gtg tcg gct gag ctc aca ggg aga cat aag ggg 528
 Ala Tyr Gly Thr Ile Val Ser Ala Glu Leu Thr Gly Arg His Lys Gly
 165 170 175
 ccc ttg gca gaa aga gac ttc aaa tca ggc cgc tgt cca ggg aac tcc 576
 Pro Leu Ala Glu Arg Asp Phe Lys Ser Gly Arg Cys Pro Gly Asn Ser
 180 185 190

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ttt tcc tgc ggg aac agc cag tgt gtg acc aag gtg aac ccg gag tgt	624
Phe Ser Cys Gly Asn Ser Gln Cys Val Thr Lys Val Asn Pro Glu Cys	
195 200 205	
gac gac cag gag gac tgc tcc gat ggg tcc gac gag gcg cac tgc gag	672
Asp Asp Gln Glu Asp Cys Ser Asp Gly Ser Asp Glu Ala His Cys Glu	
210 215 220	
tgt ggc ttg cag cct gcc tgg agg atg gcc ggc agg atc gtg ggc ggc	720
Cys Gly Leu Gln Pro Ala Trp Arg Met Ala Gly Arg Ile Val Gly Gly	
225 230 235 240	
atg gaa gca tcc ccg ggg gag ttt ccg tgg caa gcc agc ctt cga gag	768
Met Glu Ala Ser Pro Gly Glu Phe Pro Trp Gln Ala Ser Leu Arg Glu	
245 250 255	
aac aag gag cac ttc tgt ggg gcc gcc atc atc aac gcc agg tgg ctg	816
Asn Lys Glu His Phe Cys Gly Ala Ala Ile Ile Asn Ala Arg Trp Leu	
260 265 270	
gtg tct gct gct cac tgc ttc aat gag ttc caa gac ccg acg aag tgg	864
Val Ser Ala Ala His Cys Phe Asn Glu Phe Gln Asp Pro Thr Lys Trp	
275 280 285	
gtg gcc tac gtg ggt gcg acc tac ctc agc ggc tgc gag gcc agc acc	912
Val Ala Tyr Val Gly Ala Thr Tyr Leu Ser Gly Ser Glu Ala Ser Thr	
290 295 300	
gtg cgg gcc cag gtg gtc cag atc gtc aag cac ccc ctg tac aac gcg	960
Val Arg Ala Gln Val Val Gln Ile Val Lys His Pro Leu Tyr Asn Ala	
305 310 315 320	
gac acg gcc gac ttt gac gtg gct gtg ctg gag ctg acc agc cct ctg	1008
Asp Thr Ala Asp Phe Asp Val Ala Val Leu Glu Leu Thr Ser Pro Leu	
325 330 335	
cct ttc ggc ccg cac atc cag ccc gtg tgc ctc ccg gct gcc aca cac	1056
Pro Phe Gly Arg His Ile Gln Pro Val Cys Leu Pro Ala Ala Thr His	
340 345 350	
atc ttc cca ccc agc aag aag tgc ctg atc tca ggc tgg ggc tac ctc	1104
Ile Phe Pro Pro Ser Lys Lys Cys Leu Ile Ser Gly Trp Gly Tyr Leu	
355 360 365	
aag gag gac ttc ctg gtc aag cca ggg gtg ctg cag aaa gcc act gtg	1152
Lys Glu Asp Phe Leu Val Lys Pro Gly Val Leu Gln Lys Ala Thr Val	
370 375 380	
gag ctg ctg gac cag gca ctg tgt gcc agc ttg tac ggc cat tca ctc	1200
Glu Leu Leu Asp Gln Ala Leu Cys Ala Ser Leu Tyr Gly His Ser Leu	
385 390 395 400	
act gac agg atg gtg tgc gct ggc tac ctg gac ggg aag gtg gac tcc	1248
Thr Asp Arg Met Val Cys Ala Gly Tyr Leu Asp Gly Lys Val Asp Ser	
405 410 415	
tgc cag ggt gac tca gga gga ccc ctg gtc tgc gag gag ccc tct ggc	1296
Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Glu Glu Pro Ser Gly	
420 425 430	
cgg ttc tct ctg gct ggc atc gtg agc tgg gga atc ggg tgt gcg gaa	1344

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Arg	Phe	Ser	Leu	Ala	Gly	Ile	Val	Ser	Trp	Gly	Ile	Gly	Cys	Ala	Glu		
		435					440					445					
gcc	cgg	cgt	cca	ggg	gtc	tat	gcc	cga	gtc	acc	agg	cta	cgt	gac	tgg	1392	
Ala	Arg	Arg	Pro	Gly	Val	Tyr	Ala	Arg	Val	Thr	Arg	Leu	Arg	Asp	Trp		
		450				455					460						
atc	ctg	gag	gcc	acc	acc	aaa	gcc	agc	atg	cct	ctg	gcc	ccc	acc	atg	1440	
Ile	Leu	Glu	Ala	Thr	Thr	Lys	Ala	Ser	Met	Pro	Leu	Ala	Pro	Thr	Met		
		465			470					475					480		
gct	cct	gcc	cct	gcc	gcc	ccc	agc	aca	gcc	tgg	ccc	acc	agt	cct	gag	1488	
Ala	Pro	Ala	Pro	Ala	Ala	Pro	Ser	Thr	Ala	Trp	Pro	Thr	Ser	Pro	Glu		
				485					490						495		
u																	
agc	cct	gtt	gtc	agc	acc	ccc	acc	aaa	tcg	atg	cag	gcc	ctc	agt	acc	1536	
Ser	Pro	Val	Val	Ser	Thr	Pro	Thr	Lys	Ser	Met	Gln	Ala	Leu	Ser	Thr		
			500					505					510				
gtg	cct	ctt	gac	tgg	gtc	acc	gtt	cct	aag	cta	caa	gaa	tgt	ggg	gcc	1584	
Val	Pro	Leu	Asp	Trp	Val	Thr	Val	Pro	Lys	Leu	Gln	Glu	Cys	Gly	Ala		
		515					520					525					
agg	cct	gca	atg	gag	aag	ccc	acc	cgg	gtc	gtg	ggc	ggg	ttc	gga	gct	1632	
Arg	Pro	Ala	Met	Glu	Lys	Pro	Thr	Arg	Val	Val	Gly	Gly	Phe	Gly	Ala		
		530				535					540						
gcc	tcc	ggg	gag	gtg	ccc	tgg	cag	gtc	agc	ctg	aag	gaa	ggg	tcc	cgg	1680	
Ala	Ser	Gly	Glu	Val	Pro	Trp	Gln	Val	Ser	Leu	Lys	Glu	Gly	Ser	Arg		
		545			550					555					560		
cac	ttc	tgc	gga	gca	act	gtg	gtg	ggg	gac	cgc	tgg	ctg	ctg	tct	gcc	1728	
His	Phe	Cys	Gly	Ala	Thr	Val	Val	Gly	Asp	Arg	Trp	Leu	Leu	Ser	Ala		
			565					570						575			
gcc	cac	tgc	ttc	aac	cac	acg	aag	gtg	gag	cag	gtt	cgg	gcc	cac	ctg	1776	
Ala	His	Cys	Phe	Asn	His	Thr	Lys	Val	Glu	Gln	Val	Arg	Ala	His	Leu		
			580				585					590					
ggc	act	gcg	tcc	ctc	ctg	ggc	ctg	ggc	ggg	agc	ccg	gtg	aag	atc	ggg	1824	
Gly	Thr	Ala	Ser	Leu	Leu	Gly	Leu	Gly	Gly	Ser	Pro	Val	Lys	Ile	Gly		
		595				600						605					
ctg	cgg	cgg	gta	gtg	ctg	cac	ccc	ctc	tac	aac	cct	ggc	atc	ctg	gac	1872	
Leu	Arg	Arg	Val	Val	Leu	His	Pro	Leu	Tyr	Asn	Pro	Gly	Ile	Leu	Asp		
		610				615					620						
ttc	gac	ctg	gct	gtc	ctg	gag	ctg	gcc	agc	ccc	ctg	gcc	ttc	aac	aaa	1920	
Phe	Asp	Leu	Ala	Val	Leu	Glu	Leu	Ala	Ser	Pro	Leu	Ala	Phe	Asn	Lys		
		625			630					635					640		
tac	atc	cag	cct	gtc	tgc	ctg	ccc	ctg	gcc	atc	cgg	aag	ttc	cct	gtg	1968	
Tyr	Ile	Gln	Pro	Val	Cys	Leu	Pro	Leu	Ala	Ile	Arg	Lys	Phe	Pro	Val		
			645					650						655			
ggc	cgg	aag	tgc	atg	atc	tcc	gga	tgg	gga	aat	acg	cag	gaa	gga	aat	2016	
Gly	Arg	Lys	Cys	Met	Ile	Ser	Gly	Trp	Gly	Asn	Thr	Gln	Glu	Gly	Asn		
			660				665						670				
gcc	acc	aag	ccc	gag	ctc	ctg	cag	aag	gcg	tcc	gtg	ggc	atc	ata	gac	2064	
Ala	Thr	Lys	Pro	Glu	Leu	Leu	Gln	Lys	Ala	Ser	Val	Gly	Ile	Ile	Asp		

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675	680	685	
cag aaa acc tgt agt gtg ctc tac aac ttc tcc ctc aca gac cgc atg Gln Lys Thr Cys Ser Val Leu Tyr Asn Phe Ser Leu Thr Asp Arg Met 690 695 700			2112
atc tgc gca ggc ttc ctg gaa ggc aaa gtc gac tcc tgc cag ggt gac Ile Cys Ala Gly Phe Leu Glu Gly Lys Val Asp Ser Cys Gln Gly Asp 705 710 715 720			2160
tct ggg ggc ccc ctg gcc tgc gag gag gcc cct ggc gtg ttt tat ctg Ser Gly Gly Pro Leu Ala Cys Glu Glu Ala Pro Gly Val Phe Tyr Leu 725 730 735			2208
gca ggg atc gtg agc tgg ggt att ggc tgc gct cag gtt aag aag ccg Ala Gly Ile Val Ser Trp Gly Ile Gly Cys Ala Gln Val Lys Lys Pro 740 745 750			2256
ggc gtg tac acg cgc atc acc agg cta aag ggc tgg atc ctg gag atc Gly Val Tyr Thr Arg Ile Thr Arg Leu Lys Gly Trp Ile Leu Glu Ile 755 760 765			2304
atg tcc tcc cag ccc ctt ccc atg tct ccc ccc tcg acc aca agg atg Met Ser Ser Gln Pro Leu Pro Met Ser Pro Pro Ser Thr Thr Arg Met 770 775 780			2352
ctg gcc acc acc agc ccc agg acg aca gct ggc ctc aca gtc ccg ggc Leu Ala Thr Thr Ser Pro Arg Thr Thr Ala Gly Leu Thr Val Pro Gly 785 790 795 800			2400
gcc aca ccc agc aga ccc acc cct ggg gct gcc agc agg gtg acg ggc Ala Thr Pro Ser Arg Pro Thr Pro Gly Ala Ala Ser Arg Val Thr Gly 805 810 815			2448
caa cct gcc aac tca acc tta tct gcc gtg agc acc act gct agg gga Gln Pro Ala Asn Ser Thr Leu Ser Ala Val Ser Thr Thr Ala Arg Gly 820 825 830			2496
cag acg cca ttt cca gac gcc ccg gag gcc acc aca cac acc cag cta Gln Thr Pro Phe Pro Asp Ala Pro Glu Ala Thr Thr His Thr Gln Leu 835 840 845			2544
cca gac tgt ggc ctg gcg ccg gcc gcg ctc acc agg att gtg ggc ggc Pro Asp Cys Gly Leu Ala Pro Ala Ala Leu Thr Arg Ile Val Gly Gly 850 855 860			2592
agc gca gcg ggc cgt ggg gag tgg ccg tgg cag gtg ggc ctg tgg ctg Ser Ala Ala Gly Arg Gly Glu Trp Pro Trp Gln Val Gly Leu Trp Leu 865 870 875 880			2640
cgg cgc cgg gaa cac cgt tgc ggg gcc gtg ctg gtg gca gag agg tgg Arg Arg Arg Glu His Arg Cys Gly Ala Val Leu Val Ala Glu Arg Trp 885 890 895			2688
ctg ctg tcg gcg gcg cac tgc ttc gac gtc tac ggg gac ccc aag cag Leu Leu Ser Ala Ala His Cys Phe Asp Val Tyr Gly Asp Pro Lys Gln 900 905 910			2736
tgg gcg gcc ttc cta ggc acg ccg ttc ctg agc ggc gcg gag ggg cag Trp Ala Ala Phe Leu Gly Thr Pro Phe Leu Ser Gly Ala Glu Gly Gln 915 920 925			2784

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ctg gag cgc gtg gcg cgc atc tac aag cac ccg ttc tac aat ctc tac	2832
Leu Glu Arg Val Ala Arg Ile Tyr Lys His Pro Phe Tyr Asn Leu Tyr	
930 935 940	
acg ctc gac tac gac gtg gcg ctt ctg gag ctg gcg ggg ccg gtg cgt	2880
Thr Leu Asp Tyr Asp Val Ala Leu Leu Glu Leu Ala Gly Pro Val Arg	
945 950 955 960	
cgc agc cgc ctg gtg cgt ccc atc tgc ctg ccc gag ccc gcg ccg cga	2928
Arg Ser Arg Leu Val Arg Pro Ile Cys Leu Pro Glu Pro Ala Pro Arg	
965 970 975	
ccc ccg gac ggc acg cgc tgc gtc atc acc ggc tgg ggc tgc gtg cgc	2976
Pro Pro Asp Gly Thr Arg Cys Val Ile Thr Gly Trp Gly Ser Val Arg	
980 985 990	
gaa gga ggc tcc atg gcg cgg cag ctg cag aag gcg gcc gtg cgc ctc	3024
Glu Gly Gly Ser Met Ala Arg Gln Leu Gln Lys Ala Ala Val Arg Leu	
995 1000 1005	
ctc agc gag cag acc tgc cgc cgc ttc tac cca gtg cag atc agc agc	3072
Leu Ser Glu Gln Thr Cys Arg Arg Phe Tyr Pro Val Gln Ile Ser Ser	
1010 1015 1020	
cgc atg ctg tgt gcc ggc ttc ccg cag ggt ggc gtg gac agc tgc tgc	3120
Arg Met Leu Cys Ala Gly Phe Pro Gln Gly Gly Val Asp Ser Cys Ser	
1025 1030 1035 1040	
ggt gac gct ggg gga ccc ctg gcc tgc agg gag ccc tct gga cgg tgg	3168
Gly Asp Ala Gly Gly Pro Leu Ala Cys Arg Glu Pro Ser Gly Arg Trp	
1045 1050 1055	
gtg cta act ggg gtc act agc tgg ggc tat ggc tgt ggc cgg ccc cac	3216
Val Leu Thr Gly Val Thr Ser Trp Gly Tyr Gly Cys Gly Arg Pro His	
1060 1065 1070	
ttc cca ggt gtc tat acc cgg gtg gca gct gtg aga ggc tgg ata gga	3264
Phe Pro Gly Val Tyr Thr Arg Val Ala Val Arg Gly Trp Ile Gly	
1075 1080 1085	
cag cac atc cag gag tga ccaccacgtg actgccagg ccgagactct	3312
Gln His Ile Gln Glu *	
1090	
acgt	3316
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<211> 1093	
<212> PRT	
<213> Homo Sapien	
<400> 20	
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1 5 10 15	
Glu Val Pro Ala Leu Asp Ala Ala Cys Cys Arg Ala Ala Thr Ile Gly	
20 25 30	
Val Val Ala Thr Ser Leu Val Val Leu Thr Leu Gly Val Leu Leu Ala	
35 40 45	
Phe Leu Ser Thr Gln Gly Phe His Val Asp His Thr Ala Glu Leu Arg	
50 55 60	

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Gly Ile Arg Trp Thr Ser Ser Leu Arg Arg Glu Thr Ser Asp Tyr His
 65 70 75 80
 Arg Thr Leu Thr Pro Thr Leu Glu Ala Leu Phe Val Ser Ser Phe Gln
 85 90 95
 Lys Thr Glu Leu Glu Ala Ser Cys Val Gly Cys Ser Val Leu Asn Tyr
 100 105 110
 Arg Asp Gly Asn Ser Ser Val Leu Val His Phe Gln Leu His Phe Leu
 115 120 125
 Leu Arg Pro Leu Gln Thr Leu Ser Leu Gly Leu Glu Glu Glu Leu Leu
 130 135 140
 Gln Arg Gly Ile Arg Ala Arg Leu Arg Glu His Gly Ile Ser Leu Ala
 145 150 155 160
 Ala Tyr Gly Thr Ile Val Ser Ala Glu Leu Thr Gly Arg His Lys Gly
 165 170 175
 Pro Leu Ala Glu Arg Asp Phe Lys Ser Gly Arg Cys Pro Gly Asn Ser
 180 185 190
 Phe Ser Cys Gly Asn Ser Gln Cys Val Thr Lys Val Asn Pro Glu Cys
 195 200 205
 Asp Asp Gln Glu Asp Cys Ser Asp Gly Ser Asp Glu Ala His Cys Glu
 210 215 220
 Cys Gly Leu Gln Pro Ala Trp Arg Met Ala Gly Arg Ile Val Gly Gly
 225 230 235 240
 Met Glu Ala Ser Pro Gly Glu Phe Pro Trp Gln Ala Ser Leu Arg Glu
 245 250 255
 Asn Lys Glu His Phe Cys Gly Ala Ala Ile Ile Asn Ala Arg Trp Leu
 260 265 270
 Val Ser Ala Ala His Cys Phe Asn Glu Phe Gln Asp Pro Thr Lys Trp
 275 280 285
 Val Ala Tyr Val Gly Ala Thr Tyr Leu Ser Gly Ser Glu Ala Ser Thr
 290 295 300
 Val Arg Ala Gln Val Val Gln Ile Val Lys His Pro Leu Tyr Asn Ala
 305 310 315 320
 Asp Thr Ala Asp Phe Asp Val Ala Val Leu Glu Leu Thr Ser Pro Leu
 325 330 335
 Pro Phe Gly Arg His Ile Gln Pro Val Cys Leu Pro Ala Ala Thr His
 340 345 350
 Ile Phe Pro Pro Ser Lys Lys Cys Leu Ile Ser Gly Trp Gly Tyr Leu
 355 360 365
 Lys Glu Asp Phe Leu Val Lys Pro Gly Val Leu Gln Lys Ala Thr Val
 370 375 380
 Glu Leu Leu Asp Gln Ala Leu Cys Ala Ser Leu Tyr Gly His Ser Leu
 385 390 395 400
 Thr Asp Arg Met Val Cys Ala Gly Tyr Leu Asp Gly Lys Val Asp Ser
 405 410 415
 Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Glu Glu Pro Ser Gly
 420 425 430
 Arg Phe Ser Leu Ala Gly Ile Val Ser Trp Gly Ile Gly Cys Ala Glu
 435 440 445
 Ala Arg Arg Pro Gly Val Tyr Ala Arg Val Thr Arg Leu Arg Asp Trp
 450 455 460
 Ile Leu Glu Ala Thr Thr Lys Ala Ser Met Pro Leu Ala Pro Thr Met
 465 470 475 480
 Ala Pro Ala Pro Ala Ala Pro Ser Thr Ala Trp Pro Thr Ser Pro Glu
 485 490 495
 Ser Pro Val Val Ser Thr Pro Thr Lys Ser Met Gln Ala Leu Ser Thr
 500 505 510
 Val Pro Leu Asp Trp Val Thr Val Pro Lys Leu Gln Glu Cys Gly Ala
 515 520 525
 Arg Pro Ala Met Glu Lys Pro Thr Arg Val Val Gly Gly Phe Gly Ala
 530 535 540
 Ala Ser Gly Glu Val Pro Trp Gln Val Ser Leu Lys Glu Gly Ser Arg

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545					550					555				560
His	Phe	Cys	Gly	Ala	Thr	Val	Val	Gly	Asp	Arg	Trp	Leu	Leu	Ser
				565					570					575
Ala	His	Cys	Phe	Asn	His	Thr	Lys	Val	Glu	Gln	Val	Arg	Ala	His
			580					585					590	
Gly	Thr	Ala	Ser	Leu	Leu	Gly	Leu	Gly	Gly	Ser	Pro	Val	Lys	Ile
		595					600					605		
Leu	Arg	Arg	Val	Val	Leu	His	Pro	Leu	Tyr	Asn	Pro	Gly	Ile	Leu
	610				615					620				
Phe	Asp	Leu	Ala	Val	Leu	Glu	Leu	Ala	Ser	Pro	Leu	Ala	Phe	Asn
625				630						635				640
Tyr	Ile	Gln	Pro	Val	Cys	Leu	Pro	Leu	Ala	Ile	Arg	Lys	Phe	Pro
			645						650					655
Gly	Arg	Lys	Cys	Met	Ile	Ser	Gly	Trp	Gly	Asn	Thr	Gln	Glu	Gly
			660				665						670	
Ala	Thr	Lys	Pro	Glu	Leu	Leu	Gln	Lys	Ala	Ser	Val	Gly	Ile	Ile
		675					680					685		
Gln	Lys	Thr	Cys	Ser	Val	Leu	Tyr	Asn	Phe	Ser	Leu	Thr	Asp	Arg
	690					695					700			
Ile	Cys	Ala	Gly	Phe	Leu	Glu	Gly	Lys	Val	Asp	Ser	Cys	Gln	Gly
705				710						715				720
Ser	Gly	Gly	Pro	Leu	Ala	Cys	Glu	Glu	Ala	Pro	Gly	Val	Phe	Tyr
			725						730					735
Ala	Gly	Ile	Val	Ser	Trp	Gly	Ile	Gly	Cys	Ala	Gln	Val	Lys	Lys
		740					745					750		
Gly	Val	Tyr	Thr	Arg	Ile	Thr	Arg	Leu	Lys	Gly	Trp	Ile	Leu	Glu
	755					760					765			
Met	Ser	Ser	Gln	Pro	Leu	Pro	Met	Ser	Pro	Pro	Ser	Thr	Thr	Arg
	770				775						780			
Leu	Ala	Thr	Thr	Ser	Pro	Arg	Thr	Thr	Ala	Gly	Leu	Thr	Val	Pro
785				790					795					800
Ala	Thr	Pro	Ser	Arg	Pro	Thr	Pro	Gly	Ala	Ala	Ser	Arg	Val	Thr
			805						810					815
Gln	Pro	Ala	Asn	Ser	Thr	Leu	Ser	Ala	Val	Ser	Thr	Thr	Ala	Arg
		820						825					830	
Gln	Thr	Pro	Phe	Pro	Asp	Ala	Pro	Glu	Ala	Thr	Thr	His	Thr	Gln
	835						840					845		
Pro	Asp	Cys	Gly	Leu	Ala	Pro	Ala	Ala	Leu	Thr	Arg	Ile	Val	Gly
	850					855					860			
Ser	Ala	Ala	Gly	Arg	Gly	Glu	Trp	Pro	Trp	Gln	Val	Gly	Leu	Trp
865					870					875				880
Arg	Arg	Arg	Glu	His	Arg	Cys	Gly	Ala	Val	Leu	Val	Ala	Glu	Arg
			885						890					895
Leu	Leu	Ser	Ala	Ala	His	Cys	Phe	Asp	Val	Tyr	Gly	Asp	Pro	Lys
		900					905					910		
Trp	Ala	Ala	Phe	Leu	Gly	Thr	Pro	Phe	Leu	Ser	Gly	Ala	Glu	Gly
		915					920					925		
Leu	Glu	Arg	Val	Ala	Arg	Ile	Tyr	Lys	His	Pro	Phe	Tyr	Asn	Leu
	930				935						940			
Thr	Leu	Asp	Tyr	Asp	Val	Ala	Leu	Leu	Glu	Leu	Ala	Gly	Pro	Val
945				950						955				960
Arg	Ser	Arg	Leu	Val	Arg	Pro	Ile	Cys	Leu	Pro	Glu	Pro	Ala	Pro
			965						970					975
Pro	Pro	Asp	Gly	Thr	Arg	Cys	Val	Ile	Thr	Gly	Trp	Gly	Ser	Val
			980					985					990	
Glu	Gly	Gly	Ser	Met	Ala	Arg	Gln	Leu	Gln	Lys	Ala	Ala	Val	Arg
	995						1000					1005		
Leu	Ser	Glu	Gln	Thr	Cys	Arg	Arg	Phe	Tyr	Pro	Val	Gln	Ile	Ser
	1010					1015					1020			
Arg	Met	Leu	Cys	Ala	Gly	Phe	Pro	Gln	Gly	Gly	Val	Asp	Ser	Cys
1025					1030					1035				1040

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Gly Asp Ala Gly Gly Pro Leu Ala Cys Arg Glu Pro Ser Gly Arg Trp
 1045 1050 1055
 Val Leu Thr Gly Val Thr Ser Trp Gly Tyr Gly Cys Gly Arg Pro His
 1060 1065 1070
 Phe Pro Gly Val Tyr Thr Arg Val Ala Ala Val Arg Gly Trp Ile Gly
 1075 1080 1085
 Gln His Ile Gln Glu
 1090

<210> 21
 <211> 702
 <212> DNA
 <213> Homo Sapien

<220>
 <221> CDS
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 <223> Nucleic Acid encoding protease domain of
 endotheliase 1

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 Arg Ile Val Gly Gly Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln
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 gct agc ctg cag tgg gat ggg agt cat cgc tgt gga gca acc tta att 96
 Ala Ser Leu Gln Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile
 20 25 30
 aat gcc aca tgg ctt gtg agt gct gct cac tgt ttt aca aca tat aag 144
 Asn Ala Thr Trp Leu Val Ser Ala Ala His Cys Phe Thr Thr Tyr Lys
 35 40 45
 aac cct gcc aga tgg act gct tcc ttt gga gta aca ata aaa cct tcg 192
 Asn Pro Ala Arg Trp Thr Ala Ser Phe Gly Val Thr Ile Lys Pro Ser
 50 55 60
 aaa atg aaa cgg ggt ctc cgg aga ata att gtc cat gaa aaa tac aaa 240
 Lys Met Lys Arg Gly Leu Arg Arg Ile Ile His Glu Lys Tyr Lys
 65 70 75 80
 cac cca tca cat gac tat gat att tct ctt gca gag ctt tct agc cct 288
 His Pro Ser His Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser Pro
 85 90 95
 gtt ccc tac aca aat gca gta cat aga gtt tgt ctc cct gat gca tcc 336
 Val Pro Tyr Thr Asn Ala Val His Arg Val Cys Leu Pro Asp Ala Ser
 100 105 110
 tat gag ttt caa cca ggt gat gtg atg ttt gtg aca gga ttt gga gca 384
 Tyr Glu Phe Gln Pro Gly Asp Val Met Phe Val Thr Gly Phe Gly Ala
 115 120 125
 ctg aaa aat gat ggt tac agt caa aat cat ctt cga caa gca cag gtg 432
 Leu Lys Asn Asp Gly Tyr Ser Gln Asn His Leu Arg Gln Ala Gln Val
 130 135 140
 act ctc ata gac gct aca act tgc aat gaa cct caa gct tac aat gac 480
 Thr Leu Ile Asp Ala Thr Thr Cys Asn Glu Pro Gln Ala Tyr Asn Asp
 145 150 155 160

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gcc ata act cct aga atg tta tgt gct ggc tcc tta gaa gga aaa aca      528
Ala Ile Thr Pro Arg Met Leu Cys Ala Gly Ser Leu Glu Gly Lys Thr
                      165                      170                      175

gat gca tgc cag ggt gac tct gga gga cca ctg gtt agt tca gat gct      576
Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Ser Ser Asp Ala
                      180                      185                      190

aga gat atc tgg tac ctt gct gga ata gtg agc tgg gga gat gaa tgt      624
Arg Asp Ile Trp Tyr Leu Ala Gly Ile Val Ser Trp Gly Asp Glu Cys
                      195                      200                      205

gcg aaa ccc aac aag cct ggt gtt tat act aga gtt acg gcc ttg cgg      672
Ala Lys Pro Asn Lys Pro Gly Val Tyr Thr Arg Val Thr Ala Leu Arg
                      210                      215                      220

gac tgg att act tca aaa act ggt atc taa      702
Asp Trp Ile Thr Ser Lys Thr Gly Ile
225                      230

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<210> 22
<211> 233
<212> PRT
<213> Homo Sapien

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<220>
<221> SITE
<222> (1)...(233)
<223> Protease domain of endotheliase 1

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Ala Ser Leu Gln Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile
 20      25      30
Asn Ala Thr Trp Leu Val Ser Ala Ala His Cys Phe Thr Thr Tyr Lys
 35      40      45
Asn Pro Ala Arg Trp Thr Ala Ser Phe Gly Val Thr Ile Lys Pro Ser
 50      55      60
Lys Met Lys Arg Gly Leu Arg Arg Ile Ile Val His Glu Lys Tyr Lys
 65      70      75      80
His Pro Ser His Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser Pro
 85      90      95
Val Pro Tyr Thr Asn Ala Val His Arg Val Cys Leu Pro Asp Ala Ser
100     105     110
Tyr Glu Phe Gln Pro Gly Asp Val Met Phe Val Thr Gly Phe Gly Ala
115     120     125
Leu Lys Asn Asp Gly Tyr Ser Gln Asn His Leu Arg Gln Ala Gln Val
130     135     140
Thr Leu Ile Asp Ala Thr Thr Cys Asn Glu Pro Gln Ala Tyr Asn Asp
145     150     155     160
Ala Ile Thr Pro Arg Met Leu Cys Ala Gly Ser Leu Glu Gly Lys Thr
165     170     175
Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Ser Ser Asp Ala
180     185     190
Arg Asp Ile Trp Tyr Leu Ala Gly Ile Val Ser Trp Gly Asp Glu Cys
195     200     205
Ala Lys Pro Asn Lys Pro Gly Val Tyr Thr Arg Val Thr Ala Leu Arg
210     215     220
Asp Trp Ile Thr Ser Lys Thr Gly Ile

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225

230

<210> 23

<211> 1689

<212> DNA

<213> Homo Sapien

<220>

<221> CDS

<222> (1)...(1689)

<223> Nucleic acid encoding Endotheliase 2-S protein

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gct gga gca tct cca gcc cag gca tct cca gct ggg aca cct cca ggc	96
Ala Gly Ala Ser Pro Ala Gln Ala Ser Pro Ala Gly Thr Pro Pro Gly	
20 25 30	
cgg gca tct cca gcc cag gca tct cca gcc cag gca tct cca gct ggg	144
Arg Ala Ser Pro Ala Gln Ala Ser Pro Ala Gln Ala Ser Pro Ala Gly	
35 40 45	
aca cct ccg ggc cgg gca tct cca gcc cag gca tct cca gct ggt aca	192
Thr Pro Pro Gly Arg Ala Ser Pro Ala Gln Ala Ser Pro Ala Gly Thr	
50 55 60	
cct cca ggc cgg gca tct cca gcc cgg gca tct cca gcc cag gca tct	240
Pro Pro Gly Arg Ala Ser Pro Gly Arg Ala Ser Pro Ala Gln Ala Ser	
65 70 75 80	
cca gcc cgg gca tct ccg gct ctg gca tca ctt tcc agg tcc tca tcc	288
Pro Ala Arg Ala Ser Pro Ala Leu Ala Ser Leu Ser Arg Ser Ser Ser	
85 90 95	
ggc agg tca tca tcc gcc agg tca gcc tcg gtg aca acc tcc cca acc	336
Gly Arg Ser Ser Ser Ala Arg Ser Ala Ser Val Thr Thr Ser Pro Thr	
100 105 110	
aga gtg tac ctt gtt aga gca aca cca gtg ggg gct gta ccc atc cga	384
Arg Val Tyr Leu Val Arg Ala Thr Pro Val Gly Ala Val Pro Ile Arg	
115 120 125	
tca tct cct gcc agg tca gca cca gca acc agg gcc acc agg gag agc	432
Ser Ser Pro Ala Arg Ser Ala Pro Ala Thr Arg Ala Thr Arg Glu Ser	
130 135 140	
cca ggt acg agc ctg ccc aag ttc acc tgg cgg gag ggc cag aag cag	480
Pro Gly Thr Ser Leu Pro Lys Phe Thr Trp Arg Glu Gly Gln Lys Gln	
145 150 155 160	
cta ccg ctc atc ggg tgc gtg ctc ctc ctc att gcc ctg gtg gtt tcg	528
Leu Pro Leu Ile Gly Cys Val Leu Leu Leu Ile Ala Leu Val Val Ser	
165 170 175	
ctc atc atc ctc ttc cag ttc tgg cag ggc cac aca ggg atc agg tac	576
Leu Ile Ile Leu Phe Gln Phe Trp Gln Gly His Thr Gly Ile Arg Tyr	
180 185 190	

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aag gag cag agg gag agc tgt ccc aag cac gct gtt cgc tgt gac ggg Lys Glu Gln Arg Glu Ser Cys Pro Lys His Ala Val Arg Cys Asp Gly 195 200 205	624
gtg gtg gac tgc aag ctg aag agt gac gag ctg ggc tgc gtg agg ttt Val Val Asp Cys Lys Leu Lys Ser Asp Glu Leu Gly Cys Val Arg Phe 210 215 220	672
gac tgg gac aag tct ctg ctt aaa atc tac tct ggg tcc tcc cat cag Asp Trp Asp Lys Ser Leu Leu Lys Ile Tyr Ser Gly Ser Ser His Gln 225 230 235 240	720
tgg ctt ccc atc tgt agc agc aac tgg aat gac tcc tac tca gag aag Trp Leu Pro Ile Cys Ser Ser Asn Trp Asn Asp Ser Tyr Ser Glu Lys 245 250 255	768
acc tgc cag cag ctg ggt ttc gag agt gct cac cgg aca acc gag gtt Thr Cys Gln Gln Leu Gly Phe Glu Ser Ala His Arg Thr Thr Glu Val 260 265 270	816
gcc cac agg gat ttt gcc aac agc ttc tca atc ttg aga tac aac tcc Ala His Arg Asp Phe Ala Asn Ser Phe Ser Ile Leu Arg Tyr Asn Ser 275 280 285	864
acc atc cag gaa agc ctc cac agg tct gaa tgc cct tcc cag cgg tat Thr Ile Gln Glu Ser Leu His Arg Ser Glu Cys Pro Ser Gln Arg Tyr 290 295 300	912
atc tcc ctc cag tgt tcc cac tgc gga ctg agg gcc atg acc ggg cgg Ile Ser Leu Gln Cys Ser His Cys Gly Leu Arg Ala Met Thr Gly Arg 305 310 315 320	960
atc gtg gga ggg gcg ctg gcc tcg gat agc aag tgg cct tgg caa gtg Ile Val Gly Gly Ala Leu Ala Ser Asp Ser Lys Trp Pro Trp Gln Val 325 330 335	1008
agt ctg cac ttc ggc acc acc cac atc tgt gga ggc acg ctc att gac Ser Leu His Phe Gly Thr Thr His Ile Cys Gly Gly Thr Leu Ile Asp 340 345 350	1056
gcc cag tgg gtg ctc act gcc gcc cac tgc ttc ttc gtg acc cgg gag Ala Gln Trp Val Leu Thr Ala Ala His Cys Phe Phe Val Thr Arg Glu 355 360 365	1104
aag gtc ctg gag ggc tgg aag gtg tac gcg ggc acc agc aac ctg cac Lys Val Leu Glu Gly Trp Lys Val Tyr Ala Gly Thr Ser Asn Leu His 370 375 380	1152
cag ttg cct gag gca gcc tcc att gcc gag atc atc atc aac agc aat Gln Leu Pro Glu Ala Ala Ser Ile Ala Glu Ile Ile Ile Asn Ser Asn 385 390 395 400	1200
tac acc gat gag gag gac gac tat gac atc gcc ctc atg cgg ctg tcc Tyr Thr Asp Glu Glu Asp Asp Tyr Asp Ile Ala Leu Met Arg Leu Ser 405 410 415	1248
aag ccc ctg acc ctg tcc gct cac atc cac cct gct tgc ctc ccc atg Lys Pro Leu Thr Leu Ser Ala His Ile His Pro Ala Cys Leu Pro Met 420 425 430	1296

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cat gga cag acc ttt agc ctc aat gag acc tgc tgg atc aca ggc ttt      1344
His Gly Gln Thr Phe Ser Leu Asn Glu Thr Cys Trp Ile Thr Gly Phe
      435              440              445

ggc aag acc agg gag aca gat gac aag aca tcc ccc ttc ctc cgg gag      1392
Gly Lys Thr Arg Glu Thr Asp Asp Lys Thr Ser Pro Phe Leu Arg Glu
      450              455              460

gtg cag gtc aat ctc atc gac ttc aag aaa tgc aat gac tac ttg gtc      1440
Val Gln Val Asn Leu Ile Asp Phe Lys Lys Cys Asn Asp Tyr Leu Val
      465              470              475              480

tat gac agt tac ctt acc cca agg atg atg tgt gct ggg gac ctt cgt      1488
Tyr Asp Ser Tyr Leu Thr Pro Arg Met Met Cys Ala Gly Asp Leu Arg
      485              490              495

ggg ggc aga gac tcc tgc cag gga gac agc ggg ggg cct ctt gtc tgt      1536
Gly Gly Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys
      500              505              510

gag cag aac aac cgc tgg tac ctg gca ggt gtc acc agc tgg ggc aca      1584
Glu Gln Asn Asn Arg Trp Tyr Leu Ala Gly Val Thr Ser Trp Gly Thr
      515              520              525

ggc tgt ggc cag aga aac aaa cct ggt gtg tac acc aaa gtg aca gaa      1632
Gly Cys Gly Gln Arg Asn Lys Pro Gly Val Tyr Thr Lys Val Thr Glu
      530              535              540

gtt ctt ccc tgg att tac agc aag atg gag agc gag gtg cga ttc ata      1680
Val Leu Pro Trp Ile Tyr Ser Lys Met Glu Ser Glu Val Arg Phe Ile
      545              550              555              560

aaa tcc taa
Lys Ser *
      1689

<210> 24
<211> 562
<212> PRT
<213> homo sapien

<220>
<221> protease domain of endotheliase 2
<222> (321)..(562)

<400> 4
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Ala Gly Ala Ser Pro Ala Gln Ala Ser Pro Ala Gly Thr Pro Pro Gly
      20              25              30
Arg Ala Ser Pro Ala Gln Ala Ser Pro Ala Gln Ala Ser Pro Ala Gly
      35              40              45
Thr Pro Pro Gly Arg Ala Ser Pro Ala Gln Ala Ser Pro Ala Gly Thr
      50              55              60
Pro Pro Gly Arg Ala Ser Pro Gly Arg Ala Ser Pro Ala Gln Ala Ser
      65              70              75              80
Pro Ala Arg Ala Ser Pro Ala Leu Ala Ser Leu Ser Arg Ser Ser Ser
      85              90              95
Gly Arg Ser Ser Ala Arg Ser Ala Ser Val Thr Thr Ser Pro Thr
      100              105              110
Arg Val Tyr Leu Val Arg Ala Thr Pro Val Gly Ala Val Pro Ile Arg
      115              120              125

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Ser Ser Pro Ala Arg Ser Ala Pro Ala Thr Arg Ala Thr Arg Glu Ser
 130 135 140
 Pro Gly Thr Ser Leu Pro Lys Phe Thr Trp Arg Glu Gly Gln Lys Gln
 145 150 155 160
 Leu Pro Leu Ile Gly Cys Val Leu Leu Leu Ile Ala Leu Val Val Ser
 165 170 175
 Leu Ile Ile Leu Phe Gln Phe Trp Gln Gly His Thr Gly Ile Arg Tyr
 180 185 190
 Lys Glu Gln Arg Glu Ser Cys Pro Lys His Ala Val Arg Cys Asp Gly
 195 200 205
 Val Val Asp Cys Lys Leu Lys Ser Asp Glu Leu Gly Cys Val Arg Phe
 210 215 220
 Asp Trp Asp Lys Ser Leu Leu Lys Ile Tyr Ser Gly Ser Ser His Gln
 225 230 235 240
 Trp Leu Pro Ile Cys Ser Ser Asn Trp Asn Asp Ser Tyr Ser Glu Lys
 245 250 255
 Thr Cys Gln Gln Leu Gly Phe Glu Ser Ala His Arg Thr Thr Glu Val
 260 265 270
 Ala His Arg Asp Phe Ala Asn Ser Phe Ser Ile Leu Arg Tyr Asn Ser
 275 280 285
 Thr Ile Gln Glu Ser Leu His Arg Ser Glu Cys Pro Ser Gln Arg Tyr
 290 295 300
 Ile Ser Leu Gln Cys Ser His Cys Gly Leu Arg Ala Met Thr Gly Arg
 305 310 315 320
 Ile Val Gly Gly Ala Leu Ala Ser Asp Ser Lys Trp Pro Trp Gln Val
 325 330 335
 Ser Leu His Phe Gly Thr Thr His Ile Cys Gly Gly Thr Leu Ile Asp
 340 345 350
 Ala Gln Trp Val Leu Thr Ala Ala His Cys Phe Phe Val Thr Arg Glu
 355 360 365
 Lys Val Leu Glu Gly Trp Lys Val Tyr Ala Gly Thr Ser Asn Leu His
 370 375 380
 Gln Leu Pro Glu Ala Ala Ser Ile Ala Glu Ile Ile Ile Asn Ser Asn
 385 390 395 400
 Tyr Thr Asp Glu Glu Asp Asp Tyr Asp Ile Ala Leu Met Arg Leu Ser
 405 410 415
 Lys Pro Leu Thr Leu Ser Ala His Ile His Pro Ala Cys Leu Pro Met
 420 425 430
 His Gly Gln Thr Phe Ser Leu Asn Glu Thr Cys Trp Ile Thr Gly Phe
 435 440 445
 Gly Lys Thr Arg Glu Thr Asp Asp Lys Thr Ser Pro Phe Leu Arg Glu
 450 455 460
 Val Gln Val Asn Leu Ile Asp Phe Lys Lys Cys Asn Asp Tyr Leu Val
 465 470 475 480
 Tyr Asp Ser Tyr Leu Thr Pro Arg Met Met Cys Ala Gly Asp Leu Arg
 485 490 495
 Gly Gly Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys
 500 505 510
 Glu Gln Asn Asn Arg Trp Tyr Leu Ala Gly Val Thr Ser Trp Gly Thr
 515 520 525
 Gly Cys Gly Gln Arg Asn Lys Pro Gly Val Tyr Thr Lys Val Thr Glu
 530 535 540
 Val Leu Pro Trp Ile Tyr Ser Lys Met Glu Ser Glu Val Arg Phe Ile
 545 550 555 560
 Lys Ser

<210> 25

<211> 2067

<212> DNA

<213> Homo Sapien

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<220>

<221> CDS

<222> (1)...(2067)

<223> Nucleic acid encoding (endotheliase 2-L) protein

<400> 25

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Met Glu Arg Asp Ser His Gly Asn Ala Ser Pro Ala Arg Thr Pro Ser	
1 5 10 15	
gct gga gca tct cca gcc cag gca tct cca gct ggg aca cct cca ggc	96
Ala Gly Ala Ser Pro Ala Gln Ala Ser Pro Ala Gly Thr Pro Pro Gly	
20 25 30	
cgg gca tct cca gcc cag gca tct cca gcc cag gca tct cca gct ggg	144
Arg Ala Ser Pro Ala Gln Ala Ser Pro Ala Gln Ala Ser Pro Ala Gly	
35 40 45	
aca cct ccg ggc cgg gca tct cca gcc cag gca tct cca gct ggt aca	192
Thr Pro Pro Gly Arg Ala Ser Pro Ala Gln Ala Ser Pro Ala Gly Thr	
50 55 60	
cct cca ggc cgg gca tct cca gcc cgg gca tct cca gcc cag gca tct	240
Pro Pro Gly Arg Ala Ser Pro Gly Arg Ala Ser Pro Ala Gln Ala Ser	
65 70 75 80	
cca gcc cgg gca tct ccg gct ctg gca tca ctt tcc agg tcc tca tcc	288
Pro Ala Arg Ala Ser Pro Ala Leu Ala Ser Leu Ser Arg Ser Ser Ser	
85 90 95	
ggc agg tca tca tcc gcc agg tca gcc tcg gtg aca acc tcc cca acc	336
Gly Arg Ser Ser Ala Arg Ser Ala Ser Val Thr Thr Ser Pro Thr	
100 105 110	
aga gtg tac ctt gtt aga gca aca cca gtg ggg gct gta ccc atc cga	384
Arg Val Tyr Leu Val Arg Ala Thr Pro Val Gly Ala Val Pro Ile Arg	
115 120 125	
tca tct cct gcc agg tca gca cca gca acc agg gcc acc agg gag agc	432
Ser Ser Pro Ala Arg Ser Ala Pro Ala Thr Arg Ala Thr Arg Glu Ser	
130 135 140	
cca ggt acg agc ctg ccc aag ttc acc tgg cgg gag ggc cag aag cag	480
Pro Gly Thr Ser Leu Pro Lys Phe Thr Trp Arg Glu Gly Gln Lys Gln	
145 150 155 160	
cta ccg ctc atc ggg tgc gtg ctc ctc ctc att gcc ctg gtg gtt tcg	528
Leu Pro Leu Ile Gly Cys Val Leu Leu Leu Ile Ala Leu Val Val Ser	
165 170 175	
ctc atc atc ctc ttc cag ttc tgg cag ggc cac aca ggg atc agg tac	576
Leu Ile Ile Leu Phe Gln Phe Trp Gln Gly His Thr Gly Ile Arg Tyr	
180 185 190	
aag gag cag agg gag agc tgt ccc aag cac gct gtt cgc tgt gac ggg	624
Lys Glu Gln Arg Glu Ser Cys Pro Lys His Ala Val Arg Cys Asp Gly	
195 200 205	
gtg gtg gac tgc aag ctg aag agt gac gag ctg ggc tgc gtg agg ttt	672
Val Val Asp Cys Lys Leu Lys Ser Asp Glu Leu Gly Cys Val Arg Phe	
210 215 220	

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gac tgg gac aag tct ctg ctt aaa atc tac tct ggg tcc tcc cat cag Asp Trp Asp Lys Ser Leu Leu Lys Ile Tyr Ser Gly Ser Ser His Gln 225 230 235 240	720
tgg ctt ccc atc tgt agc agc aac tgg aat gac tcc tac tca gag aag Trp Leu Pro Ile Cys Ser Ser Asn Trp Asn Asp Ser Tyr Ser Glu Lys 245 250 255	768
acc tgc cag cag ctg ggt ttc gag agt gct cac cgg aca acc gag gtt Thr Cys Gln Gln Leu Gly Phe Glu Ser Ala His Arg Thr Thr Glu Val 260 265 270	816
gcc cac agg gat ttt gcc aac agc ttc tca atc ttg aga tac aac tcc Ala His Arg Asp Phe Ala Asn Ser Phe Ser Ile Leu Arg Tyr Asn Ser 275 280 285	864
acc atc cag gaa agc ctc cac agg tct gaa tgc cct tcc cag cgg tat Thr Ile Gln Glu Ser Leu His Arg Ser Glu Cys Pro Ser Gln Arg Tyr 290 295 300	912
atc tcc ctc cag tgt tcc cac tgc gga ctg agg gcc atg acc ggg cgg Ile Ser Leu Gln Cys Ser His Cys Gly Leu Arg Ala Met Thr Gly Arg 305 310 315 320	960
atc gtg gga ggg gcg ctg gcc tcg gat agc aag tgg cct tgg caa gtg Ile Val Gly Gly Ala Leu Ala Ser Asp Ser Lys Trp Pro Trp Gln Val 325 330 335	1008
agt ctg cac ttc ggc acc acc cac atc tgt gga ggc acg ctc att gac Ser Leu His Phe Gly Thr Thr His Ile Cys Gly Gly Thr Leu Ile Asp 340 345 350	1056
gcc cag tgg gtg ctc act gcc gcc cac tgc ttc ttc gtg acc cgg gag Ala Gln Trp Val Leu Thr Ala Ala His Cys Phe Phe Val Thr Arg Glu 355 360 365	1104
aag gtc ctg gag ggc tgg aag gtg tac gcg ggc acc agc aac ctg cac Lys Val Leu Glu Gly Trp Lys Val Tyr Ala Gly Thr Ser Asn Leu His 370 375 380	1152
cag ttg cct gag gca gcc tcc att gcc gag atc atc atc aac agc aat Gln Leu Pro Glu Ala Ala Ser Ile Ala Glu Ile Ile Ile Asn Ser Asn 385 390 400	1200
tac acc gat gag gag gac gac tat gac atc gcc ctc atg cgg ctg tcc Tyr Thr Asp Glu Glu Asp Asp Tyr Asp Ile Ala Leu Met Arg Leu Ser 405 410 415	1248
aag ccc ctg acc ctg tcc gct cac atc cac cct gct tgc ctc ccc atg Lys Pro Leu Thr Leu Ser Ala His Ile His Pro Ala Cys Leu Pro Met 420 425 430	1296
cat gga cag acc ttt agc ctc aat gag acc tgc tgg atc aca ggc ttt His Gly Gln Thr Phe Ser Leu Asn Glu Thr Cys Trp Ile Thr Gly Phe 435 440 445	1344
ggc aag acc agg gag aca gat gac aag aca tcc ccc ttc ctc cgg gag Gly Lys Thr Arg Glu Thr Asp Asp Lys Thr Ser Pro Phe Leu Arg Glu 450 455 460	1392

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gtg cag gtc aat ctc atc gac ttc aag aaa tgc aat gac tac ttg gtc Val Gln Val Asn Leu Ile Asp Phe Lys Lys Cys Asn Asp Tyr Leu Val 465 470 475 480	1440
tat gac agt tac ctt acc cca agg atg atg tgt gct ggg gac ctt cgt Tyr Asp Ser Tyr Leu Thr Pro Arg Met Met Cys Ala Gly Asp Leu Arg 485 490 495	1488
ggg ggc aga gac tcc tgc cag gga gac agc ggg ggg cct ctt gtc tgt Gly Gly Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys 500 505 510	1536
gag cag aac aac cgc tgg tac ctg gca ggt gtc acc agc tgg ggc aca Glu Gln Asn Asn Arg Trp Tyr Leu Ala Gly Val Thr Ser Trp Gly Thr 515 520 525	1584
ggc tgt ggc cag aga aac aaa cct ggt gtg tac acc aaa gtg aca gaa Gly Cys Gly Gln Arg Asn Lys Pro Gly Val Tyr Thr Lys Val Thr Glu 530 535 540	1632
gtt ctt ccc tgg att tac agc aag atg gag aac aga gct cag cgg gtt Val Leu Pro Trp Ile Tyr Ser Lys Met Glu Asn Arg Ala Gln Arg Val 545 550 555 560	1680
gaa aaa gcg tgg acc tac agg cca ggc agg cag ttg ctg ggc aga tgt Glu Lys Ala Trp Thr Tyr Arg Pro Gly Arg Gln Leu Leu Gly Arg Cys 565 570 575	1728
tct ccc aga agt att ttt ttg tgt aag gtt gca atg gac ttt gaa aac Ser Pro Arg Ser Ile Phe Leu Cys Lys Val Ala Met Asp Phe Glu Asn 580 585 590	1776
gtt tca gtt tct gca gag gat ttt gtg ata gtt ttt gtt atc aag cat Val Ser Val Ser Ala Glu Asp Phe Val Ile Val Phe Val Ile Lys His 595 600 605	1824
tta tgc atg gga atc cgc tct toa tgg cct ttc cca gct ctg ttt gtt Leu Cys Met Gly Ile Arg Ser Ser Trp Pro Phe Pro Ala Leu Phe Val 610 615 620	1872
tta gtc ttt ttg att ttc ttt ttg ttg ttg ttg ttg tct ttt tta aaa Leu Val Phe Leu Ile Phe Phe Leu Leu Leu Leu Leu Ser Phe Leu Lys 625 630 635 640	1920
aac aca agt gac tcc att ttg act ctg aca act ttc aca gct gtc acc Asn Thr Ser Asp Ser Ile Leu Thr Leu Thr Phe Thr Phe Thr Ala Val Thr 645 650 655	1968
aga atg ctc cct gag aac tac cat tct ttc cct ttc cca ctt aaa ata Arg Met Leu Pro Glu Asn Tyr His Ser Phe Pro Phe Pro Leu Lys Ile 660 665 670	2016
ttt cat cag aac ctc act act atc ata aaa gag tat aaa gta ata aaa Phe His Gln Asn Leu Thr Thr Ile Ile Lys Glu Tyr Lys Val Ile Lys 675 680 685	2064
taa	2067
<210> 26	
<211> 688	
<212> PRT	

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<213> Homo Sapien

<220>

<221> protease domain

<222> (321)..(688)

<400> 26

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 20      25      30
Arg Ala Ser Pro Ala Gln Ala Ser Pro Ala Gln Ala Ser Pro Ala Gly
 35      40      45
Thr Pro Pro Gly Arg Ala Ser Pro Ala Gln Ala Ser Pro Ala Gly Thr
 50      55      60
Pro Pro Gly Arg Ala Ser Pro Gly Arg Ala Ser Pro Ala Gln Ala Ser
 65      70      75      80
Pro Ala Arg Ala Ser Pro Ala Leu Ala Ser Leu Ser Arg Ser Ser Ser
 85      90      95
Gly Arg Ser Ser Ser Ala Arg Ser Ala Ser Val Thr Thr Ser Pro Thr
 100     105     110
Arg Val Tyr Leu Val Arg Ala Thr Pro Val Gly Ala Val Pro Ile Arg
 115     120     125
Ser Ser Pro Ala Arg Ser Ala Pro Ala Thr Arg Ala Thr Arg Glu Ser
 130     135     140
Pro Gly Thr Ser Leu Pro Lys Phe Thr Trp Arg Glu Gly Gln Lys Gln
 145     150     155     160
Leu Pro Leu Ile Gly Cys Val Leu Leu Leu Ile Ala Leu Val Val Ser
 165     170     175
Leu Ile Ile Leu Phe Gln Phe Trp Gln Gly His Thr Gly Ile Arg Tyr
 180     185     190
Lys Glu Gln Arg Glu Ser Cys Pro Lys His Ala Val Arg Cys Asp Gly
 195     200     205
Val Val Asp Cys Lys Leu Lys Ser Asp Glu Leu Gly Cys Val Arg Phe
 210     215     220
Asp Trp Asp Lys Ser Leu Leu Lys Ile Tyr Ser Gly Ser Ser His Gln
 225     230     235     240
Trp Leu Pro Ile Cys Ser Ser Asn Trp Asn Asp Ser Tyr Ser Glu Lys
 245     250     255
Thr Cys Gln Gln Leu Gly Phe Glu Ser Ala His Arg Thr Thr Glu Val
 260     265     270
Ala His Arg Asp Phe Ala Asn Ser Phe Ser Ile Leu Arg Tyr Asn Ser
 275     280     285
Thr Ile Gln Glu Ser Leu His Arg Ser Glu Cys Pro Ser Gln Arg Tyr
 290     295     300
Ile Ser Leu Gln Cys Ser His Cys Gly Leu Arg Ala Met Thr Gly Arg
 305     310     315     320
Ile Val Gly Gly Ala Leu Ala Ser Asp Ser Lys Trp Pro Trp Gln Val
 325     330     335
Ser Leu His Phe Gly Thr Thr His Ile Cys Gly Gly Thr Leu Ile Asp
 340     345     350
Ala Gln Trp Val Leu Thr Ala Ala His Cys Phe Phe Val Thr Arg Glu
 355     360     365
Lys Val Leu Glu Gly Trp Lys Val Tyr Ala Gly Thr Ser Asn Leu His
 370     375     380
Gln Leu Pro Glu Ala Ala Ser Ile Ala Glu Ile Ile Asn Ser Asn
 385     390     395     400
Tyr Thr Asp Glu Glu Asp Asp Tyr Asp Ile Ala Leu Met Arg Leu Ser
 405     410     415
Lys Pro Leu Thr Leu Ser Ala His Ile His Pro Ala Cys Leu Pro Met
 420     425     430

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His Gly Gln Thr Phe Ser Leu Asn Glu Thr Cys Trp Ile Thr Gly Phe
 435 440 445
 Gly Lys Thr Arg Glu Thr Asp Asp Lys Thr Ser Pro Phe Leu Arg Glu
 450 455 460
 Val Gln Val Asn Leu Ile Asp Phe Lys Lys Cys Asn Asp Tyr Leu Val
 465 470 475 480
 Tyr Asp Ser Tyr Leu Thr Pro Arg Met Met Cys Ala Gly Asp Leu Arg
 485 490 495
 Gly Gly Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys
 500 505 510
 Glu Gln Asn Asn Arg Trp Tyr Leu Ala Gly Val Thr Ser Trp Gly Thr
 515 520 525
 Gly Cys Gly Gln Arg Asn Lys Pro Gly Val Tyr Thr Lys Val Thr Glu
 530 535 540
 Val Leu Pro Trp Ile Tyr Ser Lys Met Glu Asn Arg Ala Gln Arg Val
 545 550 555 560
 Glu Lys Ala Trp Thr Tyr Arg Pro Gly Arg Gln Leu Leu Gly Arg Cys
 565 570 575
 Ser Pro Arg Ser Ile Phe Leu Cys Lys Val Ala Met Asp Phe Glu Asn
 580 585 590
 Val Ser Val Ser Ala Glu Asp Phe Val Ile Val Phe Val Ile Lys His
 595 600 605
 Leu Cys Met Gly Ile Arg Ser Ser Trp Pro Phe Pro Ala Leu Phe Val
 610 615 620
 Leu Val Phe Leu Ile Phe Phe Leu Leu Leu Leu Ser Phe Leu Lys
 625 630 635 640
 Asn Thr Ser Asp Ser Ile Leu Thr Leu Thr Thr Phe Thr Ala Val Thr
 645 650 655
 Arg Met Leu Pro Glu Asn Tyr His Ser Phe Pro Phe Pro Leu Lys Ile
 660 665 670
 Phe His Gln Asn Leu Thr Thr Ile Ile Lys Glu Tyr Lys Val Ile Lys
 675 680 685

<210> 27

<211> 1471

<212> DNA

<213> Homo Sapien

<220>

<223> DESC1 gene

<221> misc feature

<222> (626)...(1324)

<223> protease domain

<221> CDS

<222> (56)...(1324)

<400> 27

tgacttggat gtagacctcg accttcacag gactcttcat tgctggttgg caatg atg
 Met
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58

tat cgg cca gat gtg gtg agg gct agg aaa aga gtt tgt tgg gaa ccc
 Tyr Arg Pro Asp Val Val Arg Ala Arg Lys Arg Val Cys Trp Glu Pro
 5 10 15

106

tgg gtt atc ggc ctc gtc ats ttc ata tcc ctg att gtc ctg gca gtg
 Trp Val Ile Gly Leu Val Xaa Phe Ile Ser Leu Ile Val Leu Ala Val
 20 25 30

154

-51-

tgc att gga stc act gtt cat tat gtg aga tat aat caa aag aag acc Cys Ile Gly Xaa Thr Val His Tyr Val Arg Tyr Asn Gln Lys Lys Thr 35 40 45	202
tac aat tac tat agc aca ttg tca ttt aca act gac aaa cta tat gct Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr Thr Asp Lys Leu Tyr Ala 50 55 60 65	250
gag ttt ggc aga gag gct tct aac aat ttt aca gaa atg agc cag aga Glu Phe Gly Arg Glu Ala Ser Asn Asn Phe Thr Glu Met Ser Gln Arg 70 75 80	298
ctt gaa tca atg gtg aaa aat gca ttt tat aaa tct cca tta agg gaa Leu Glu Ser Met Val Lys Asn Ala Phe Tyr Lys Ser Pro Leu Arg Glu 85 90 95	346
gaa ttt gtc aag tct cag gtt atc aag ttc agt caa cag aag cat gga Glu Phe Val Lys Ser Gln Val Ile Lys Phe Ser Gln Gln Lys His Gly 100 105 110	394
gtg ttg gct cat atg ctg ttg att tgt aga ttt cac tct act gag gat Val Leu Ala His Met Leu Leu Ile Cys Arg Phe His Ser Thr Glu Asp 115 120 125	442
cct gaa act gta gat aaa att gtt caa ctt gtt tta cat gaa aag ctg Pro Glu Thr Val Asp Lys Ile Val Gln Leu Val Leu His Glu Lys Leu 130 135 140 145	490
caa gat gct gta gga ccc cct aaa gta gat cct cac tca gtt aaa att Gln Asp Ala Val Gly Pro Pro Lys Val Asp Pro His Ser Val Lys Ile 150 155 160	538
aaa aaa atc aac aag aca gaa aca gac agc tat cta aac cat tgc tgc Lys Lys Ile Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys Cys 165 170 175	586
gga aca cga aga agt aaa act cta ggt cag agt ctc agg atc gtt ggt Gly Thr Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val Gly 180 185 190	634
ggg aca gaa gta gaa gag ggt gaa tgg ccc tgg cag gct agc ctg cag Gly Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln 195 200 205	682
tgg gat ggg agt cat cgc tgt gga gca acc tta att aat gcc aca tgg Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile Asn Ala Thr Trp 210 215 220 225	730
ctt gtg agt gct gct cac tgt ttt aca aca tat aag aac cct gcc aga Leu Val Ser Ala Ala His Cys Phe Thr Thr Tyr Lys Asn Pro Ala Arg 230 235 240	778
tgg act gct tcc ttt gga gta aca ata aaa cct tgc aaa atg aaa cgg Trp Thr Ala Ser Phe Gly Val Thr Ile Lys Pro Ser Lys Met Lys Arg 245 250 255	826
ggt ctc cgg aga ata att gtc cat gaa aaa tac aaa cac cca tca cat Gly Leu Arg Arg Ile Ile Val His Glu Lys Tyr Lys His Pro Ser His 260 265 270	874
gac tat gat att tct ctt gca gag ctt tct agc cct gtt ccc tac aca	922

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Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser Pro Val Pro Tyr Thr
275                280                285

aat gca gta cat aga gtt tgt ctc cct gat gca tcc tat gag ttt caa      970
Asn Ala Val His Arg Val Cys Leu Pro Asp Ala Ser Tyr Glu Phe Gln
290                295                300                305

cca ggt gat gtg atg ttt gtg aca gga ttt gga gca ctg aaa aat gat      1018
Pro Gly Asp Val Met Phe Val Thr Gly Phe Gly Ala Leu Lys Asn Asp
310                315                320

ggt tac agt caa aat cat ctt cga caa gca cag gtg act ctc ata gac      1066
Gly Tyr Ser Gln Asn His Leu Arg Gln Ala Gln Val Thr Leu Ile Asp
325                330                335

gct aca act tgc aat gaa cct caa gct tac aat gac gcc ata act cct      1114
Ala Thr Thr Cys Asn Glu Pro Gln Ala Tyr Asn Asp Ala Ile Thr Pro
340                345                350

aga atg tta tgt gct ggc tcc tta gaa gga aaa aca gat gca tgc cag      1162
Arg Met Leu Cys Ala Gly Ser Leu Glu Gly Lys Thr Asp Ala Cys Gln
355                360                365

ggt gac tct gga gga cca ctg gtt agt tca gat gct aga gat atc tgg      1210
Gly Asp Ser Gly Gly Pro Leu Val Ser Ser Asp Ala Arg Asp Ile Trp
370                375                380                385

tac ctt gct gga ata gtg agc tsg gga gat gaa tgt gcg aaa ccc aac      1258
Tyr Leu Ala Gly Ile Val Ser Xaa Gly Asp Glu Cys Ala Lys Pro Asn
390                395                400

aag cct ggt gtt tat act aga gtt acg gcc ttg cgg gac tgg att act      1306
Lys Pro Gly Val Tyr Thr Arg Val Thr Ala Leu Arg Asp Trp Ile Thr
405                410                415

tca aaa act ggt atc taa gagagaaaag cctcatggaa cagataacat      1354
Ser Lys Thr Gly Ile *
420

ttttttttgt tttttgggtg tggaggccat ttttagagat acagaattgg agaagacttg      1414
caaaacagct agatttgact gatctcaata aactgtttgc ttgatgcaaa aaaaaaa      1471

<210> 28
<211> 4933
<212> DNA
<213> Homo Sapien

<220>
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<222> (94)...(3222)
<223> Nucleotide sequence encoding corin

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<308> GenBank AF133845
<309> 1999-05-24

<400> 28
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agtggacaga agaataagcg agacttttta tcc atg aaa cag tct cct gcc ctc      114
Met Lys Gln Ser Pro Ala Leu
1 5

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-53-

gct ccg gaa gag cgc tac cgc aga gcc ggg tcc cca aag ccg gtc ttg Ala Pro Glu Glu Arg Tyr Arg Arg Ala Gly Ser Pro Lys Pro Val Leu 10 15 20	162
aga gct gat gac aat aac atg ggc aat ggc tgc tct cag aag ctg gcg Arg Ala Asp Asp Asn Asn Met Gly Asn Gly Cys Ser Gln Lys Leu Ala 25 30 35	210
act gct aac ctc ctc cgg ttc cta ttg ctg gtc ctg att cca tgt atc Thr Ala Asn Leu Leu Arg Phe Leu Leu Leu Val Leu Ile Pro Cys Ile 40 45 50 55	258
tgt gct ctc gtt ctc ttg ctg gtg atc ctg ctt tcc tat gtt gga aca Cys Ala Leu Val Leu Leu Leu Val Ile Leu Leu Ser Tyr Val Gly Thr 60 65 70	306
tta caa aag gtc tat ttt aaa tca aat ggg agt gaa cct ttg gtc act Leu Gln Lys Val Tyr Phe Lys Ser Asn Gly Ser Glu Pro Leu Val Thr 75 80 85	354
gat ggt gaa atc caa ggg tcc gat gtt att ctt aca aat aca att tat Asp Gly Glu Ile Gln Gly Ser Asp Val Ile Leu Thr Asn Thr Ile Tyr 90 95 100	402
aac cag agc act gtg gtg tct act gca cat ccc gac caa cac gtt cca Asn Gln Ser Thr Val Val Ser Thr Ala His Pro Asp Gln His Val Pro 105 110 115	450
gcc tgg act acg gat gct tct ctc cca ggg gac caa agt cac agg aat Ala Trp Thr Thr Asp Ala Ser Leu Pro Gly Asp Gln Ser His Arg Asn 120 125 130 135	498
aca agt gcc tgt atg aac atc acc cac agc cag tgt cag atg ctg ccc Thr Ser Ala Cys Met Asn Ile Thr His Ser Gln Cys Gln Met Leu Pro 140 145 150	546
tac cac gcc acg ctg aca cct ctc ctc tca gtt gtc aga aac atg gaa Tyr His Ala Thr Leu Thr Pro Leu Leu Ser Val Val Arg Asn Met Glu 155 160 165	594
atg gaa aag ttc ctc aag ttt ttc aca tat ctc cat cgc ctc agt tgc Met Glu Lys Phe Leu Lys Phe Phe Thr Tyr Leu His Arg Leu Ser Cys 170 175 180	642
tat caa cat atc atg ctg ttt ggc tgt acc ctc gcc ttc cct gag tgc Tyr Gln His Ile Met Leu Phe Gly Cys Thr Leu Ala Phe Pro Glu Cys 185 190 195	690
atc att gat ggc gat gac agt cat gga ctc ctg ccc tgt agg tcc ttc Ile Ile Asp Gly Asp Asp Ser His Gly Leu Leu Pro Cys Arg Ser Phe 200 205 210 215	738
tgt gag gct gca aaa gaa ggc tgt gaa tca gtc ctg ggg atg gtg aat Cys Glu Ala Ala Lys Glu Gly Cys Glu Ser Val Leu Gly Met Val Asn 220 225 230	786
tac tcc tgg ccg gat ttc ctc aga tgc tcc cag ttt aga aac caa act Tyr Ser Trp Pro Asp Phe Leu Arg Cys Ser Gln Phe Arg Asn Gln Thr 235 240 245	834

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gaa agc agc aat gtc agc aga att tgc ttc tca cct cag cag gaa aac Glu Ser Ser Asn Val Ser Arg Ile Cys Phe Ser Pro Gln Gln Glu Asn 250 255 260	882
gga aag caa ttg ctc tgt gga agg ggt gag aac ttt ctg tgt gcc agt Gly Lys Gln Leu Leu Cys Gly Arg Gly Glu Asn Phe Leu Cys Ala Ser 265 270 275	930
gga atc tgc atc ccc ggg aaa ctg caa tgt aat ggc tac aac gac tgt Gly Ile Cys Ile Pro Gly Lys Leu Gln Cys Asn Gly Tyr Asn Asp Cys 280 285 290 295	978
gac gac tgg agt gac gag gct cat tgc aac tgc agc gag aat ctg ttt Asp Asp Trp Ser Asp Glu Ala His Cys Asn Cys Ser Glu Asn Leu Phe 300 305 310	1026
cac tgt cac aca ggc aag tgc ctt aat tac agc ctt gtg tgt gat gga His Cys His Thr Gly Lys Cys Leu Asn Tyr Ser Leu Val Cys Asp Gly 315 320 325	1074
tat gat gac tgt ggg gat ttg agt gat gag caa aac tgt gat tgc aat Tyr Asp Asp Cys Gly Asp Leu Ser Asp Glu Gln Asn Cys Asp Cys Asn 330 335 340	1122
ccc aca aca gag cat cgc tgc ggg gac ggg cgc tgc atc gcc atg gag Pro Thr Thr Glu His Arg Cys Gly Asp Gly Arg Cys Ile Ala Met Glu 345 350 355	1170
tgg gtg tgt gat ggt gac cac gac tgt gtg gat aag tcc gac gag gtc Trp Val Cys Asp Gly Asp His Asp Cys Val Asp Lys Ser Asp Glu Val 360 365 370 375	1218
aac tgc tcc tgt cac agc cag ggt ctg gtg gaa tgc aga aat gga caa Asn Cys Ser Cys His Ser Gln Gly Leu Val Glu Cys Arg Asn Gly Gln 380 385 390	1266
tgt atc ccc agc acg ttt caa tgt gat ggt gac gag gac tgc aag gat Cys Ile Pro Ser Thr Phe Gln Cys Asp Gly Asp Glu Asp Cys Lys Asp 395 400 405	1314
ggg agt gat gag gag aac tgc agc gtc att cag act tca tgt caa gaa Gly Ser Asp Glu Glu Asn Cys Ser Val Ile Gln Thr Ser Cys Gln Glu 410 415 420	1362
gga gac caa aga tgc ctc tac aat ccc tgc ctt gat tca tgt ggt ggt Gly Asp Gln Arg Cys Leu Tyr Asn Pro Cys Leu Asp Ser Cys Gly Gly 425 430 435	1410
agc tct ctc tgt gac ccg aac aac agt ctg aat aac tgt agt caa tgt Ser Ser Leu Cys Asp Pro Asn Asn Ser Leu Asn Asn Cys Ser Gln Cys 440 445 450 455	1458
gaa cca att aca ttg gaa ctc tgc atg aat ttg ccc tac aac agt aca Glu Pro Ile Thr Leu Glu Leu Cys Met Asn Leu Pro Tyr Asn Ser Thr 460 465 470	1506
agt tat cca aat tat ttt ggc cac agg act caa aag gaa gca tcc atc Ser Tyr Pro Asn Tyr Phe Gly His Arg Thr Gln Lys Glu Ala Ser Ile 475 480 485	1554
agc tgg gag tct tct ctt ttc cct gca ctt gtt caa acc aac tgt tat	1602

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Ser	Trp	Glu	Ser	Ser	Leu	Phe	Pro	Ala	Leu	Val	Gln	Thr	Asn	Cys	Tyr	
		490					495					500				
aaa	tac	ctc	atg	ttc	ttt	tct	tgc	acc	att	ttg	gta	cca	aaa	tgt	gat	1650
Lys	Tyr	Leu	Met	Phe	Phe	Ser	Cys	Thr	Ile	Leu	Val	Pro	Lys	Cys	Asp	
	505					510					515					
gtg	aat	aca	ggc	gag	cgt	atc	cct	cct	tgc	agg	gca	ttg	tgt	gaa	cac	1698
Val	Asn	Thr	Gly	Glu	Arg	Ile	Pro	Pro	Cys	Arg	Ala	Leu	Cys	Glu	His	
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tct	aaa	gaa	cgc	tgt	gag	tct	gtt	ctt	ggg	att	gtg	ggc	cta	cag	tgg	1746
Ser	Lys	Glu	Arg		Glu	Ser	Val	Leu	Gly	Ile	Val	Gly	Leu	Gln	Trp	
				540					545					550		
cct	gaa	gac	aca	gat	tgc	agt	caa	ttt	cca	gag	gaa	aat	tca	gac	aat	1794
Pro	Glu	Asp		Thr	Asp	Cys	Ser	Gln	Phe	Pro	Glu	Glu	Asn	Ser	Asp	
			555					560					565			
caa	acc	tgc	ctg	atg	cct	gat	gaa	tat	gtg	gaa	gaa	tgc	tca	cct	agt	1842
Gln	Thr	Cys	Leu	Met	Pro	Asp	Glu	Tyr	Val	Glu	Glu	Cys	Ser	Pro	Ser	
		570					575					580				
cat	ttc	aag	tgc	cgc	tca	gga	cag	tgt	gtt	ctg	gct	tcc	aga	aga	tgt	1890
His	Phe	Lys	Cys	Arg	Ser	Gly	Gln	Cys	Val	Leu	Ala	Ser	Arg	Arg	Cys	
	585					590					595					
gat	ggc	cag	gcc	gac	tgt	gac	gat	gac	agt	gat	gag	gaa	aac	tgt	ggt	1938
Asp	Gly	Gln	Ala	Asp	Cys	Asp	Asp	Asp	Ser	Asp	Glu	Glu	Asn	Cys	Gly	
	600				605					610					615	
tgt	aaa	gag	aga	gat	ctt	tgg	gaa	tgt	cca	tcc	aat	aaa	caa	tgt	ttg	1986
Cys	Lys	Glu	Arg	Asp	Leu	Trp	Glu	Cys	Pro	Ser	Asn	Lys	Gln	Cys	Leu	
				620					625					630		
aag	cac	aca	gtg	atc	tgc	gat	ggg	ttc	cca	gac	tgc	cct	gat	tac	atg	2034
Lys	His	Thr	Val	Ile	Cys	Asp	Gly	Phe	Pro	Asp	Cys	Pro	Asp	Tyr	Met	
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gac	gag	aaa	aac	tgc	tca	ttt	tgc	caa	gat	gat	gag	ctg	gaa	tgt	gca	2082
Asp	Glu	Lys	Asn	Cys	Ser	Phe	Cys	Gln	Asp	Asp	Glu	Leu	Glu	Cys	Ala	
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Asn	His	Ala	Cys	Val	Ser	Arg	Asp	Leu	Trp	Cys	Asp	Gly	Glu	Ala	Asp	
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tgc	tca	gac	agt	tca	gat	gaa	tgg	gac	tgt	gtg	acc	ctc	tct	ata	aat	2178
Cys	Ser	Asp	Ser	Ser	Asp	Glu	Trp	Asp	Cys	Val	Thr	Leu	Ser	Ile	Asn	
	680				685					690					695	
gtg	aac	tcc	tct	tcc	ttt	ctg	atg	gtt	cac	aga	gct	gcc	aca	gaa	cac	2226
Val	Asn	Ser	Ser	Ser	Phe	Leu	Met	Val	His	Arg	Ala	Ala	Thr	Glu	His	
				700					705					710		
cat	gtg	tgt	gca	gat	ggc	tgg	cag	gag	ata	ttg	agt	cag	ctg	gcc	tgc	2274
His	Val	Cys	Ala	Asp	Gly	Trp	Gln	Glu	Ile	Leu	Ser	Gln	Leu	Ala	Cys	
			715					720					725			
aag	cag	atg	ggt	tta	gga	gaa	cca	tct	gtg	acc	aaa	ttg	ata	cag	gaa	2322
Lys	Gln	Met	Gly	Leu	Gly	Glu	Pro	Ser	Val	Thr	Lys	Leu	Ile	Gln	Glu	

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730	735	740	
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ctc aat ggg acc act tta cat gaa ctt cta gta aat ggg cag tct tgt Leu Asn Gly Thr Thr Leu His Glu Leu Leu Val Asn Gly Gln Ser Cys 760 765 770 775			2418
gag agc aga agt aaa att tct ctt ctg tgt act aaa caa gac tgt ggg Glu Ser Arg Ser Lys Ile Ser Leu Leu Cys Thr Lys Gln Asp Cys Gly 780 785 790			2466
cgc cgc cct gct gcc cga atg aac aaa agg atc ctt gga ggt cgg acg Arg Arg Pro Ala Ala Arg Met Asn Lys Arg Ile Leu Gly Gly Arg Thr 795 800 805			2514
agt cgc cct gga agg tgg cca tgg cag tgt tct ctg cag agt gaa ccc Ser Arg Pro Gly Arg Trp Pro Trp Gln Cys Ser Leu Gln Ser Glu Pro 810 815 820			2562
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aca gtt gcc cac tgc ttc gag ggg aga gag aat gct gca gtt tgg aaa Thr Val Ala His Cys Phe Glu Gly Arg Glu Asn Ala Ala Val Trp Lys 840 845 850 855			2658
gtg gtg ctt ggc atc aac aat cta gac cat cca tca gtg ttc atg cag Val Val Leu Gly Ile Asn Asn Leu Asp His Pro Ser Val Phe Met Gln 860 865 870			2706
aca cgc ttt gtg aag acc atc atc ctg cat ccc cgc tac agt cga gca Thr Arg Phe Val Lys Thr Ile Ile Leu His Pro Arg Tyr Ser Arg Ala 875 880 885			2754
gtg gtg gac tat gac atc agc atc gtt gag ctg agt gaa gac atc agt Val Val Asp Tyr Asp Ile Ser Ile Val Glu Leu Ser Glu Asp Ile Ser 890 895 900			2802
gag act ggc tac gtc cgg cct gtc tgc ttg ccc aac ccg gag cag tgg Glu Thr Gly Tyr Val Arg Pro Val Cys Leu Pro Asn Pro Glu Gln Trp 905 910 915			2850
cta gag cct gac acg tac tgc tat atc aca ggc tgg ggc cac atg ggc Leu Glu Pro Asp Thr Tyr Cys Tyr Ile Thr Gly Trp Gly His Met Gly 920 925 930 935			2898
aat aaa atg cca ttt aag ctg caa gag gga gag gtc cgc att att tct Asn Lys Met Pro Phe Lys Leu Gln Glu Gly Glu Val Arg Ile Ile Ser 940 945 950			2946
ctg gaa cat tgt cag tcc tac ttt gac atg aag acc atc acc act cgg Leu Glu His Cys Gln Ser Tyr Phe Asp Met Lys Thr Ile Thr Thr Arg 955 960 965			2994
atg ata tgt gct ggc tat gag tct ggc aca gtt gat tca tgc atg ggt Met Ile Cys Ala Gly Tyr Glu Ser Gly Thr Val Asp Ser Cys Met Gly 970 975 980			3042

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Asp Ser Gly Gly Pro Leu Val Cys Glu Lys Pro Gly Gly Arg Trp Thr
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tta ttt gga tta act tca tgg ggc tcc gtc tgc ttt tcc aaa gtc ctg 3138
Leu Phe Gly Leu Thr Ser Trp Gly Ser Val Cys Phe Ser Lys Val Leu
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Gly Pro Gly Val Tyr Ser Asn Val Ser Tyr Phe Val Glu Trp Ile Lys
                1020                1025                1030

aga cag att tac atc cag acc ttt ctc cta aac taa ttataaggat 3232
Arg Gln Ile Tyr Ile Gln Thr Phe Leu Leu Asn *
                1035                1040

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<212> PRT

<213> Homo Sapien

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Gly Ser Pro Lys Pro Val Leu Arg Ala Asp Asp Asn Asn Met Gly Asn
                20          25          30
Gly Cys Ser Gln Lys Leu Ala Thr Ala Asn Leu Leu Arg Phe Leu Leu
                35          40          45
Leu Val Leu Ile Pro Cys Ile Cys Ala Leu Val Leu Leu Leu Val Ile
 50          55          60

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Leu Leu Ser Tyr Val Gly Thr Leu Gln Lys Val Tyr Phe Lys Ser Asn
 65 70 75 80
 Gly Ser Glu Pro Leu Val Thr Asp Gly Glu Ile Gln Gly Ser Asp Val
 85 90 95
 Ile Leu Thr Asn Thr Ile Tyr Asn Gln Ser Thr Val Val Ser Thr Ala
 100 105 110
 His Pro Asp Gln His Val Pro Ala Trp Thr Thr Asp Ala Ser Leu Pro
 115 120 125
 Gly Asp Gln Ser His Arg Asn Thr Ser Ala Cys Met Asn Ile Thr His
 130 135 140
 Ser Gln Cys Gln Met Leu Pro Tyr His Ala Thr Leu Thr Pro Leu Leu
 145 150 155 160
 Ser Val Val Arg Asn Met Glu Met Glu Lys Phe Leu Lys Phe Phe Thr
 165 170 175
 Tyr Leu His Arg Leu Ser Cys Tyr Gln His Ile Met Leu Phe Gly Cys
 180 185 190
 Thr Leu Ala Phe Pro Glu Cys Ile Ile Asp Gly Asp Asp Ser His Gly
 195 200 205
 Leu Leu Pro Cys Arg Ser Phe Cys Glu Ala Ala Lys Glu Gly Cys Glu
 210 215 220
 Ser Val Leu Gly Met Val Asn Tyr Ser Trp Pro Asp Phe Leu Arg Cys
 225 230 235 240
 Ser Gln Phe Arg Asn Gln Thr Glu Ser Ser Asn Val Ser Arg Ile Cys
 245 250 255
 Phe Ser Pro Gln Gln Glu Asn Gly Lys Gln Leu Leu Cys Gly Arg Gly
 260 265 270
 Glu Asn Phe Leu Cys Ala Ser Gly Ile Cys Ile Pro Gly Lys Leu Gln
 275 280 285
 Cys Asn Gly Tyr Asn Asp Cys Asp Asp Trp Ser Asp Glu Ala His Cys
 290 295 300
 Asn Cys Ser Glu Asn Leu Phe His Cys His Thr Gly Lys Cys Leu Asn
 305 310 315 320
 Tyr Ser Leu Val Cys Asp Gly Tyr Asp Asp Cys Gly Asp Leu Ser Asp
 325 330 335
 Glu Gln Asn Cys Asp Cys Asn Pro Thr Thr Glu His Arg Cys Gly Asp
 340 345 350
 Gly Arg Cys Ile Ala Met Glu Trp Val Cys Asp Gly Asp His Asp Cys
 355 360 365
 Val Asp Lys Ser Asp Glu Val Asn Cys Ser Cys His Ser Gln Gly Leu
 370 375 380
 Val Glu Cys Arg Asn Gly Gln Cys Ile Pro Ser Thr Phe Gln Cys Asp
 385 390 395 400
 Gly Asp Glu Asp Cys Lys Asp Gly Ser Asp Glu Glu Asn Cys Ser Val
 405 410 415
 Ile Gln Thr Ser Cys Gln Glu Gly Asp Gln Arg Cys Leu Tyr Asn Pro
 420 425 430
 Cys Leu Asp Ser Cys Gly Gly Ser Ser Leu Cys Asp Pro Asn Asn Ser
 435 440 445
 Leu Asn Asn Cys Ser Gln Cys Glu Pro Ile Thr Leu Glu Leu Cys Met
 450 455 460
 Asn Leu Pro Tyr Asn Ser Thr Ser Tyr Pro Asn Tyr Phe Gly His Arg
 465 470 475 480
 Thr Gln Lys Glu Ala Ser Ile Ser Trp Glu Ser Ser Leu Phe Pro Ala
 485 490 495
 Leu Val Gln Thr Asn Cys Tyr Lys Tyr Leu Met Phe Phe Ser Cys Thr
 500 505 510
 Ile Leu Val Pro Lys Cys Asp Val Asn Thr Gly Glu Arg Ile Pro Pro
 515 520 525
 Cys Arg Ala Leu Cys Glu His Ser Lys Glu Arg Cys Glu Ser Val Leu
 530 535 540
 Gly Ile Val Gly Leu Gln Trp Pro Glu Asp Thr Asp Cys Ser Gln Phe

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545					550					555			560
Pro	Glu	Glu	Asn	Ser	Asp	Asn	Gln	Thr	Cys	Leu	Met	Pro	Asp
				565					570				Glu Tyr
Val	Glu	Glu	Cys	Ser	Pro	Ser	His	Phe	Lys	Cys	Arg	Ser	Gly
			580					585					Gln Cys
Val	Leu	Ala	Ser	Arg	Arg	Cys	Asp	Gly	Gln	Ala	Asp	Cys	Asp
		595					600					590	Asp Asp
Ser	Asp	Glu	Glu	Asn	Cys	Gly	Cys	Lys	Glu	Arg	Asp	Leu	Trp
	610					615					620		Glu Cys
Pro	Ser	Asn	Lys	Gln	Cys	Leu	Lys	His	Thr	Val	Ile	Cys	Asp
	625				630					635			Gly Phe
Pro	Asp	Cys	Pro	Asp	Tyr	Met	Asp	Glu	Lys	Asn	Cys	Ser	Phe
				645					650				Cys Gln
Asp	Asp	Glu	Leu	Glu	Cys	Ala	Asn	His	Ala	Cys	Val	Ser	Arg
			660					665					Asp Leu
Trp	Cys	Asp	Gly	Glu	Ala	Asp	Cys	Ser	Asp	Ser	Ser	Asp	Glu
		675					680					685	Trp Asp
Cys	Val	Thr	Leu	Ser	Ile	Asn	Val	Asn	Ser	Ser	Ser	Phe	Leu
	690					695					700		Met Val
His	Arg	Ala	Ala	Thr	Glu	His	His	Val	Cys	Ala	Asp	Gly	Trp
	705				710					715			Gln Glu
Ile	Leu	Ser	Gln	Leu	Ala	Cys	Lys	Gln	Met	Gly	Leu	Gly	Glu
			725						730				Pro Ser
Val	Thr	Lys	Leu	Ile	Gln	Glu	Gln	Glu	Lys	Glu	Pro	Arg	Trp
			740					745				750	Leu Thr
Leu	His	Ser	Asn	Trp	Glu	Ser	Leu	Asn	Gly	Thr	Thr	Leu	His
		755					760					765	Glu Leu
Leu	Val	Asn	Gly	Gln	Ser	Cys	Glu	Ser	Arg	Ser	Lys	Ile	Ser
	770					775					780		Leu Leu
Cys	Thr	Lys	Gln	Asp	Cys	Gly	Arg	Arg	Pro	Ala	Ala	Arg	Met
	785				790					795			Asn Lys
Arg	Ile	Leu	Gly	Gly	Arg	Thr	Ser	Arg	Pro	Gly	Arg	Trp	Pro
			805						810				Trp Gln
Cys	Ser	Leu	Gln	Ser	Glu	Pro	Ser	Gly	His	Ile	Cys	Gly	Cys
			820					825					Val Leu
Ile	Ala	Lys	Lys	Trp	Val	Leu	Thr	Val	Ala	His	Cys	Phe	Glu
		835					840					845	Gly Arg
Glu	Asn	Ala	Ala	Val	Trp	Lys	Val	Val	Leu	Gly	Ile	Asn	Asn
	850					855					860		Leu Asp
His	Pro	Ser	Val	Phe	Met	Gln	Thr	Arg	Phe	Val	Lys	Thr	Ile
	865				870					875			Ile Leu
His	Pro	Arg	Tyr	Ser	Arg	Ala	Val	Val	Asp	Tyr	Asp	Ile	Ser
				885					890				Ile Val
Glu	Leu	Ser	Glu	Asp	Ile	Ser	Glu	Thr	Gly	Tyr	Val	Arg	Pro
			900					905				910	Val Cys
Leu	Pro	Asn	Pro	Glu	Gln	Trp	Leu	Glu	Pro	Asp	Thr	Tyr	Cys
		915					920					925	Tyr Ile
Thr	Gly	Trp	Gly	His	Met	Gly	Asn	Lys	Met	Pro	Phe	Lys	Leu
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Gly	Glu	Val	Arg	Ile	Ile	Ser	Leu	Glu	His	Cys	Gln	Ser	Tyr
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Met	Lys	Thr	Ile	Thr	Thr	Arg	Met	Ile	Cys	Ala	Gly	Tyr	Glu
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Thr	Val	Asp	Ser	Cys	Met	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val
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Lys	Pro	Gly	Gly	Arg	Trp	Thr	Leu	Phe	Gly	Leu	Thr	Ser	Trp
		995					1000					1005	Gly Ser
Val	Cys	Phe	Ser	Lys	Val	Leu	Gly	Pro	Gly	Val	Tyr	Ser	Asn
	1010					1015					1020		Val Ser
Tyr	Phe	Val	Glu	Trp	Ile	Lys	Arg	Gln	Ile	Tyr	Ile	Gln	Thr
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										Met Gly Ser Lys Arg								
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ggc	ata	tct	tct	agg	cat	cat	tct	ctc	agc	tcc	tat	gaa	atc	atg	ttt			
Gly	Ile	Ser	Ser	Arg	His	His	Ser	Leu	Ser	Ser	Tyr	Glu	Ile	Met	Phe			
				10					15					20				
gca	gct	ctc	ttt	gcc	ata	ttg	gta	gtg	ctc	tgt	gct	gga	tta	att	gca			
Ala	Ala	Leu	Phe	Ala	Ile	Leu	Val	Val	Leu	Cys	Ala	Gly	Leu	Ile	Ala			
			25					30					35					
gta	tcc	tgc	ctg	aca	atc	aag	gaa	tcc	caa	cga	ggg	gca	gca	ctt	gga			
Val	Ser	Cys	Leu	Thr	Ile	Lys	Glu	Ser	Gln	Arg	Gly	Ala	Ala	Leu	Gly			
		40					45					50						
cag	agt	cat	gaa	gcc	aga	gcg	aca	ttt	aaa	ata	aca	tcc	gga	gtt	aca			
Gln	Ser	His	Glu	Ala	Arg	Ala	Thr	Phe	Lys	Ile	Thr	Ser	Gly	Val	Thr			
	55					60					65							
tat	aat	cct	aat	ttg	caa	gac	aaa	ctc	tca	gtg	gat	ttc	aaa	gtt	ctt			
Tyr	Asn	Pro	Asn	Leu	Gln	Asp	Lys	Leu	Ser	Val	Asp	Phe	Lys	Val	Leu			
	70				75				80					85				
gct	ttt	gac	ctt	cag	caa	atg	ata	gat	gag	atc	ttt	cta	tca	agc	aat			
Ala	Phe	Asp	Leu	Gln	Gln	Met	Ile	Asp	Glu	Ile	Phe	Leu	Ser	Ser	Asn			
				90					95					100				
ctg	aag	aat	gaa	tat	aag	aac	tca	aga	gtt	tta	caa	ttt	gaa	aat	ggc			
Leu	Lys	Asn	Glu	Tyr	Lys	Asn	Ser	Arg	Val	Leu	Gln	Phe	Glu	Asn	Gly			
			105				110						115					
agc	att	ata	gtc	gta	ttt	gac	ctt	ttc	ttt	gcc	cag	tgg	gtg	tca	gat			
Ser	Ile	Ile	Val	Val	Phe	Asp	Leu	Phe	Phe	Ala	Gln	Trp	Val	Ser	Asp			
		120					125					130						
caa	aat	gta	aaa	gaa	gaa	ctg	att	caa	ggc	ctt	gaa	gca	aat	aaa	tcc			
Gln	Asn	Val	Lys	Glu	Glu	Leu	Ile	Gln	Gly	Leu	Glu	Ala	Asn	Lys	Ser			
	135					140					145							
agc	caa	ctg	gtc	act	ttc	cat	att	gat	ttg	aac	agc	gtt	gat	atc	cta			
Ser	Gln	Leu	Val	Thr	Phe	His	Ile	Asp	Leu	Asn	Ser	Val	Asp	Ile	Leu			
	150				155				160						165			

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gac aag cta aca acc acc agt cat ctg gca act cca gga aat gtc tca Asp Lys Leu Thr Thr Thr Ser His Leu Ala Thr Pro Gly Asn Val Ser 170 175 180	583
ata gag tgc ctg cct ggt tca agt cct tgt act gat gct cta acg tgt Ile Glu Cys Leu Pro Gly Ser Ser Pro Cys Thr Asp Ala Leu Thr Cys 185 190 195	631
ata aaa gct gat tta ttt tgt gat gga gaa gta aac tgt cca gat ggt Ile Lys Ala Asp Leu Phe Cys Asp Gly Glu Val Asn Cys Pro Asp Gly 200 205 210	679
tct gac gaa gac aat aaa atg tgt gcc aca gtt tgt gat gga aga ttt Ser Asp Glu Asp Asn Lys Met Cys Ala Thr Val Cys Asp Gly Arg Phe 215 220 225	727
ttg tta act gga tca tct ggg tct ttc cag gct act cat tat cca aaa Leu Leu Thr Gly Ser Ser Gly Ser Phe Gln Ala Thr His Tyr Pro Lys 230 235 240 245	775
cct tct gaa aca agt gtt gtc tgc cag tgg atc ata cgt gta aac caa Pro Ser Glu Thr Ser Val Val Cys Gln Trp Ile Ile Arg Val Asn Gln 250 255 260	823
gga ctt tcc att aaa ctg agc ttc gat gat ttt aat aca tat tat aca Gly Leu Ser Ile Lys Leu Ser Phe Asp Asp Phe Asn Thr Tyr Tyr Thr 265 270 275	871
gat ata tta gat att tat gaa ggt gta gga tca agc aag att tta aga Asp Ile Leu Asp Ile Tyr Glu Gly Val Gly Ser Ser Lys Ile Leu Arg 280 285 290	919
gct tct att tgg gaa act aat cct ggc aca ata aga att ttt tcc aac Ala Ser Ile Trp Glu Thr Phe Asn Pro Gly Thr Ile Arg Ile Phe Ser Asn 295 300 305	967
caa gtt act gcc acc ttt ctt ata gaa tct gat gaa agt gat tat gtt Gln Val Thr Ala Thr Phe Leu Ile Glu Ser Asp Glu Ser Asp Tyr Val 310 315 320 325	1015
ggc ttt aat gca aca tat act gca ttt aac agc agt gag ctt aat aat Gly Phe Asn Ala Thr Tyr Thr Ala Phe Asn Ser Ser Glu Leu Asn Asn 330 335 340	1063
tat gag aaa att aat tgt aac ttt gag gat ggc ttt tgt ttc tgg gtc Tyr Glu Lys Ile Asn Cys Asn Phe Glu Asp Gly Phe Cys Phe Trp Val 345 350 355	1111
cag gat cta aat gat gat aat gaa tgg gaa agg att cag gga agc acc Gln Asp Leu Asn Asp Asp Asn Glu Trp Glu Arg Ile Gln Gly Ser Thr 360 365 370	1159
ttt tct cct ttt act gga ccc aat ttt gac cac act ttt ggc aat gct Phe Ser Pro Phe Thr Gly Pro Asn Phe Asp His Thr Phe Gly Asn Ala 375 380 385	1207
tca gga ttt tac att tct acc cca act gga cca gga ggg aga caa gaa Ser Gly Phe Tyr Ile Ser Thr Pro Thr Gly Pro Gly Gly Arg Gln Glu 390 395 400 405	1255

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cga gtg ggg ctt tta agc ctc cct ttg gac ccc act ttg gag cca gct Arg Val Gly Leu Leu Ser Leu Pro Leu Asp Pro Thr Leu Glu Pro Ala 410 415 420	1303
tgc ctt agt ttc tgg tat cat atg tat ggt gaa aat gtc cat aaa tta Cys Leu Ser Phe Trp Tyr His Met Tyr Gly Glu Asn Val His Lys Leu 425 430 435	1351
agc att aat atc agc aat gac caa aat atg gag aag aca gtt ttc caa Ser Ile Asn Ile Ser Asn Asp Gln Asn Met Glu Lys Thr Val Phe Gln 440 445 450	1399
aag gaa gga aat tat gga gac aat tgg aat tat gga caa gta acc cta Lys Glu Gly Asn Tyr Gly Asp Asn Trp Asn Tyr Gly Gln Val Thr Leu 455 460 465	1447
aat gaa aca gtt aaa ttt aag gtt gct ttt aat gct ttt aaa aac aag Asn Glu Thr Val Lys Phe Lys Val Ala Phe Asn Ala Phe Lys Asn Lys 470 475 480 485	1495
atc ctg agt gat att gcg ttg gat gac att agc cta aca tat ggg att Ile Leu Ser Asp Ile Ala Leu Asp Asp Ile Ser Leu Thr Tyr Gly Ile 490 495 500	1543
tgc aat ggg agt ctt tat cca gaa cca act ttg gtg cca act cct cca Cys Asn Gly Ser Leu Tyr Pro Glu Pro Thr Leu Val Pro Thr Pro Pro 505 510 515	1591
cca gaa ctt cct acg gac tgt gga gga cct ttt gag ctg tgg gag cca Pro Glu Leu Pro Thr Asp Cys Gly Gly Pro Phe Glu Leu Trp Glu Pro 520 525 530	1639
aat aca aca ttc agt tct acg aac ttt cca aac agc tac cct aat ctg Asn Thr Thr Phe Ser Ser Thr Asn Phe Pro Asn Ser Tyr Pro Asn Leu 535 540 545	1687
gct ttc tgt gtt tgg att tta aat gca caa aaa gga aag aat ata caa Ala Phe Cys Val Trp Ile Leu Asn Ala Gln Lys Gly Lys Asn Ile Gln 550 555 560 565	1735
ctt cat ttt caa gaa ttt gac tta gaa aat att aac gat gta gtt gaa Leu His Phe Gln Glu Phe Asp Leu Glu Asn Ile Asn Asp Val Val Glu 570 575 580	1783
ata aga gat ggt gaa gaa gct gat tcc ttg ctc tta gct gtg tac aca Ile Arg Asp Gly Glu Glu Ala Asp Ser Leu Leu Leu Ala Val Tyr Thr 585 590 595	1831
ggg cct ggc cca gta aag gat gtg ttc tct acc acc aac aga atg act Gly Pro Gly Pro Val Lys Asp Val Phe Ser Thr Thr Asn Arg Met Thr 600 605 610	1879
gtg ctt ctc atc act aac gat gtg ttg gca aga gga ggg ttt aaa gca Val Leu Leu Ile Thr Asn Asp Val Leu Ala Arg Gly Gly Phe Lys Ala 615 620 625	1927
aac ttt act act ggc tat cac ttg ggg att cca gag cca tgc aag gca Asn Phe Thr Thr Gly Tyr His Leu Gly Ile Pro Glu Pro Cys Lys Ala 630 635 640 645	1975
gac cat ttt caa tgt aaa aat gga gag tgt gtt cca ctg gtg aat ctc	2023

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Asp His Phe Gln Cys Lys Asn Gly Glu Cys Val Pro Leu Val Asn Leu	
650 655 660	
tgt gac ggt cat ctg cac tgt gag gat ggc tca gat gaa gca gat tgt	2071
Cys Asp Gly His Leu His Cys Glu Asp Gly Ser Asp Glu Ala Asp Cys	
665 670 675	
gtg cgt ttt ttc aat ggc aca acg aac aac aat ggt tta gtg cgg ttc	2119
Val Arg Phe Phe Asn Gly Thr Thr Asn Asn Asn Gly Leu Val Arg Phe	
680 685 690	
aga atc cag agc ata tgg cat aca gct tgt gct gag aac tgg acc acc	2167
Arg Ile Gln Ser Ile Trp His Thr Ala Cys Ala Glu Asn Trp Thr Thr	
695 700 705	
cag att tca aat gat gtt tgt caa ctg ctg gga cta ggg agt gga aac	2215
Gln Ile Ser Asn Asp Val Cys Gln Leu Leu Gly Leu Gly Ser Gly Asn	
710 715 720 725	
tca tca aag cca atc ttc tct acc gat ggt gga cca ttt gtc aaa tta	2263
Ser Ser Lys Pro Phe Ser Thr Asp Gly Gly Pro Phe Val Lys Leu	
730 735 740	
aac aca gca cct gat ggc cac tta ata cta aca ccc agt caa cag tgt	2311
Asn Thr Ala Pro Asp Gly His Leu Ile Leu Thr Pro Ser Gln Gln Cys	
745 750 755	
tta cag gat tcc ttg att cgg tta cag tgt aac cat aaa tct tgt gga	2359
Leu Gln Asp Ser Leu Ile Arg Leu Gln Cys Asn His Lys Ser Cys Gly	
760 765 770	
aaa aaa ctg gca gct caa gac atc acc cca aag att gtt gga gga agt	2407
Lys Lys Leu Ala Ala Gln Asp Ile Thr Pro Lys Ile Val Gly Gly Ser	
775 780 785	
aat gcc aaa gaa ggg gcc tgg ccc tgg gtt gtg ggt ctg tat tat ggc	2455
Asn Ala Lys Glu Gly Ala Trp Pro Trp Val Val Gly Leu Tyr Tyr Gly	
790 795 800 805	
ggc cga ctg ctc tgc ggc gca tct ctc gtc agc agt gac tgg ctg gtg	2503
Gly Arg Leu Leu Cys Gly Ala Ser Leu Val Ser Ser Asp Trp Leu Val	
810 815 820	
tcc gcc gca cac tgc gtg tat ggg aga aac tta gag cca tcc aag tgg	2551
Ser Ala Ala His Cys Val Tyr Gly Arg Asn Leu Glu Pro Ser Lys Trp	
825 830 835	
aca gca atc cta ggc ctg cat atg aaa tca aat ctg acc tct cct caa	2599
Thr Ala Ile Leu Gly Leu His Met Lys Ser Asn Leu Thr Ser Pro Gln	
840 845 850	
aca gtc cct cga tta ata gat gaa att gtc ata aac cct cat tac aat	2647
Thr Val Pro Arg Leu Ile Asp Glu Ile Val Ile Asn Pro His Tyr Asn	
855 860 865	
agg cga aga aag gac aac gac att gcc atg atg cat ctg gaa ttt aaa	2695
Arg Arg Arg Lys Asp Asn Asp Ile Ala Met Met His Leu Glu Phe Lys	
870 875 880 885	
gtg aat tac aca gat tac ata caa cct att tgt tta ccg gaa gaa aat	2743
Val Asn Tyr Thr Asp Tyr Ile Gln Pro Ile Cys Leu Pro Glu Glu Asn	

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890	895	900	
caa gtt ttt cct cca gga aga aat tgt tct att gct ggt tgg ggg acg Gln Val Phe Pro Pro Gly Arg Asn Cys Ser Ile Ala Gly Trp Gly Thr 905 910 915			2791
gtt gta tat caa ggt act act gca aac ata ttg caa gaa gct gat gtt Val Val Tyr Gln Gly Thr Thr Ala Asn Ile Leu Gln Glu Ala Asp Val 920 925 930			2839
cct ctt cta tca aat gag aga tgc caa cag cag atg cca gaa tat aac Pro Leu Leu Ser Asn Glu Arg Cys Gln Gln Gln Met Pro Glu Tyr Asn 935 940 945			2887
att act gaa aat atg ata tgt gca ggc tat gaa gaa gga gga ata gat Ile Thr Glu Asn Met Ile Cys Ala Gly Tyr Glu Glu Gly Gly Ile Asp 950 955 960 965			2935
tct tgt cag ggg gat tca gga gga cca tta atg tgc caa gaa aac aac Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Met Cys Gln Glu Asn Asn 970 975 980			2983
agg tgg ttc ctt gct ggt gtg acc tca ttt gga tac aag tgt gcc ctg Arg Trp Phe Leu Ala Gly Val Thr Ser Phe Gly Tyr Lys Cys Ala Leu 985 990 995			3031
cct aat cgc ccc gga gtg tat gcc agg gtc tca agg ttt acc gaa tgg Pro Asn Arg Pro Gly Val Tyr Ala Arg Val Ser Arg Phe Thr Glu Trp 1000 1005 1010			3079
ata caa agt ttt cta cat tag cgcatttctt aaactaaaca ggaaagtgcg Ile Gln Ser Phe Leu His * 1015			3130
attatatttcc cattctactc tagaaagcat ggaaattaag tgtttcgtac aaaaatttta aaaagtacc aaagggtttt attctttacct atgtcaatga aatgctaggg ggccagggaa acaaaatttt aaaaataata aaattcacca tagcaataca gaataacttt aaaataccat taaatacatt tgtatttcat tgtgaacagg tatttcttca cagatctcat ttttaaaatt cttaattgatt atttttatta cttactgttg tttaaaggga tgttatttta aagcatatac catacactta agaaatttga gcagaattta aaaaagaaaag aaaataaatt gtttttccca aagtatgtca ctgttggaat taaactgcc aaaaattttct agttccagtt tagtttgctg ctatttagcag aaactcaatt gtttctctgt cttttctatc aaaattttca acatatgcat aaccttagta ttttcccaac caatagaaac tattttattgt aagcttatgt cacaggcctg gactaaattg attttacgtt cctctt			3190 3250 3310 3370 3430 3490 3550 3610 3670 3696
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Ala Gly Leu Ile Ala Val Ser Cys Leu Thr Ile Lys Glu Ser Gln Arg 35 40 45			
Gly Ala Ala Leu Gly Gln Ser His Glu Ala Arg Ala Thr Phe Lys Ile 50 55 60			
Thr Ser Gly Val Thr Tyr Asn Pro Asn Leu Gln Asp Lys Leu Ser Val 65 70 75 80			

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Asp Phe Lys Val Leu Ala Phe Asp Leu Gln Gln Met Ile Asp Glu Ile
 85 90 95
 Phe Leu Ser Ser Asn Leu Lys Asn Glu Tyr Lys Asn Ser Arg Val Leu
 100 105 110
 Gln Phe Glu Asn Gly Ser Ile Ile Val Val Phe Asp Leu Phe Phe Ala
 115 120 125
 Gln Trp Val Ser Asp Gln Asn Val Lys Glu Glu Leu Ile Gln Gly Leu
 130 135 140
 Glu Ala Asn Lys Ser Ser Gln Leu Val Thr Phe His Ile Asp Leu Asn
 145 150 155 160
 Ser Val Asp Ile Leu Asp Lys Leu Thr Thr Thr Ser His Leu Ala Thr
 165 170 175
 Pro Gly Asn Val Ser Ile Glu Cys Leu Pro Gly Ser Ser Pro Cys Thr
 180 185 190
 Asp Ala Leu Thr Cys Ile Lys Ala Asp Leu Phe Cys Asp Gly Glu Val
 195 200 205
 Asn Cys Pro Asp Gly Ser Asp Glu Asp Asn Lys Met Cys Ala Thr Val
 210 215 220
 Cys Asp Gly Arg Phe Leu Leu Thr Gly Ser Ser Gly Ser Phe Gln Ala
 225 230 235 240
 Thr His Tyr Pro Lys Pro Ser Glu Thr Ser Val Val Cys Gln Trp Ile
 245 250 255
 Ile Arg Val Asn Gln Gly Leu Ser Ile Lys Leu Ser Phe Asp Asp Phe
 260 265 270
 Asn Thr Tyr Tyr Thr Asp Ile Leu Asp Ile Tyr Glu Gly Val Gly Ser
 275 280 285
 Ser Lys Ile Leu Arg Ala Ser Ile Trp Glu Thr Asn Pro Gly Thr Ile
 290 295 300
 Arg Ile Phe Ser Asn Gln Val Thr Ala Thr Phe Leu Ile Glu Ser Asp
 305 310 315 320
 Glu Ser Asp Tyr Val Gly Phe Asn Ala Thr Tyr Thr Ala Phe Asn Ser
 325 330 335
 Ser Glu Leu Asn Asn Tyr Glu Lys Ile Asn Cys Asn Phe Glu Asp Gly
 340 345 350
 Phe Cys Phe Trp Val Gln Asp Leu Asn Asp Asp Asn Glu Trp Glu Arg
 355 360 365
 Ile Gln Gly Ser Thr Phe Ser Pro Phe Thr Gly Pro Asn Phe Asp His
 370 375 380
 Thr Phe Gly Asn Ala Ser Gly Phe Tyr Ile Ser Thr Pro Thr Gly Pro
 385 390 395 400
 Gly Gly Arg Gln Glu Arg Val Gly Leu Leu Ser Leu Pro Leu Asp Pro
 405 410 415
 Thr Leu Glu Pro Ala Cys Leu Ser Phe Trp Tyr His Met Tyr Gly Glu
 420 425 430
 Asn Val His Lys Leu Ser Ile Asn Ile Ser Asn Asp Gln Asn Met Glu
 435 440 445
 Lys Thr Val Phe Gln Lys Glu Gly Asn Tyr Gly Asp Asn Trp Asn Tyr
 450 455 460
 Gly Gln Val Thr Leu Asn Glu Thr Val Lys Phe Lys Val Ala Phe Asn
 465 470 475 480
 Ala Phe Lys Asn Lys Ile Leu Ser Asp Ile Ala Leu Asp Asp Ile Ser
 485 490 495
 Leu Thr Tyr Gly Ile Cys Asn Gly Ser Leu Tyr Pro Glu Pro Thr Leu
 500 505 510
 Val Pro Thr Pro Pro Pro Glu Leu Pro Thr Asp Cys Gly Gly Pro Phe
 515 520 525
 Glu Leu Trp Glu Pro Asn Thr Thr Phe Ser Ser Thr Asn Phe Pro Asn
 530 535 540
 Ser Tyr Pro Asn Leu Ala Phe Cys Val Trp Ile Leu Asn Ala Gln Lys
 545 550 555 560
 Gly Lys Asn Ile Gln Leu His Phe Gln Glu Phe Asp Leu Glu Asn Ile

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                    565                    570                    575
Asn Asp Val Val Glu Ile Arg Asp Gly Glu Glu Ala Asp Ser Leu Leu
                    580                    585                    590
Leu Ala Val Tyr Thr Gly Pro Gly Pro Val Lys Asp Val Phe Ser Thr
                    595                    600                    605
Thr Asn Arg Met Thr Val Leu Leu Ile Thr Asn Asp Val Leu Ala Arg
                    610                    615                    620
Gly Gly Phe Lys Ala Asn Phe Thr Thr Gly Tyr His Leu Gly Ile Pro
625                    630                    635                    640
Glu Pro Cys Lys Ala Asp His Phe Gln Cys Lys Asn Gly Glu Cys Val
                    645                    650                    655
Pro Leu Val Asn Leu Cys Asp Gly His Leu His Cys Glu Asp Gly Ser
                    660                    665                    670
Asp Glu Ala Asp Cys Val Arg Phe Phe Asn Gly Thr Thr Asn Asn Asn
                    675                    680                    685
Gly Leu Val Arg Phe Arg Ile Gln Ser Ile Trp His Thr Ala Cys Ala
                    690                    695                    700
Glu Asn Trp Thr Thr Gln Ile Ser Asn Asp Val Cys Gln Leu Leu Gly
705                    710                    715                    720
Leu Gly Ser Gly Asn Ser Ser Lys Pro Ile Phe Ser Thr Asp Gly Gly
                    725                    730                    735
Pro Phe Val Lys Leu Asn Thr Ala Pro Asp Gly His Leu Ile Leu Thr
                    740                    745                    750
Pro Ser Gln Gln Cys Leu Gln Asp Ser Leu Ile Arg Leu Gln Cys Asn
                    755                    760                    765
His Lys Ser Cys Gly Lys Lys Leu Ala Ala Gln Asp Ile Thr Pro Lys
                    770                    775                    780
Ile Val Gly Gly Ser Asn Ala Lys Glu Gly Ala Trp Pro Trp Val Val
785                    790                    795                    800
Gly Leu Tyr Tyr Gly Gly Arg Leu Leu Cys Gly Ala Ser Leu Val Ser
                    805                    810                    815
Ser Asp Trp Leu Val Ser Ala Ala His Cys Val Tyr Gly Arg Asn Leu
                    820                    825                    830
Glu Pro Ser Lys Trp Thr Ala Ile Leu Gly Leu His Met Lys Ser Asn
                    835                    840                    845
Leu Thr Ser Pro Gln Thr Val Pro Arg Leu Ile Asp Glu Ile Val Ile
                    850                    855                    860
Asn Pro His Tyr Asn Arg Arg Arg Lys Asp Asn Asp Ile Ala Met Met
865                    870                    875                    880
His Leu Glu Phe Lys Val Asn Tyr Thr Asp Tyr Ile Gln Pro Ile Cys
                    885                    890                    895
Leu Pro Glu Glu Asn Gln Val Phe Pro Pro Gly Arg Asn Cys Ser Ile
                    900                    905                    910
Ala Gly Trp Gly Thr Val Val Tyr Gln Gly Thr Thr Ala Asn Ile Leu
                    915                    920                    925
Gln Glu Ala Asp Val Pro Leu Ser Asn Glu Arg Cys Gln Gln Gln
                    930                    935                    940
Met Pro Glu Tyr Asn Ile Thr Glu Asn Met Ile Cys Ala Gly Tyr Glu
945                    950                    955                    960
Glu Gly Gly Ile Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Met
                    965                    970                    975
Cys Gln Glu Asn Asn Arg Trp Phe Leu Ala Gly Val Thr Ser Phe Gly
                    980                    985                    990
Tyr Lys Cys Ala Leu Pro Asn Arg Pro Gly Val Tyr Ala Arg Val Ser
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Arg Phe Thr Glu Trp Ile Gln Ser Phe Leu His
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<213> Homo Sapien

<220>

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<222> (62)...(1318)

<223> Nucleotide sequence encoding human airway
trypsin-like protease

<300>

<308> GenBank AB002134

<309> 1998-06-04

<400> 32

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a atg tat agg cca gca cgt gta act tcg act tca aga ttt ctg aat cca      109
  Met Tyr Arg Pro Ala Arg Val Thr Ser Thr Ser Arg Phe Leu Asn Pro
    1             5             10             15

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tat gta gta tgt ttc att gtc gtc gca ggg gta gtg atc ctg gca gtc      157
Tyr Val Val Cys Phe Ile Val Val Ala Gly Val Val Ile Leu Ala Val
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acc ata gct cta ctt gtt tac ttt tta gct ttt gat caa aaa tct tac      205
Thr Ile Ala Leu Leu Val Tyr Phe Leu Ala Phe Asp Gln Lys Ser Tyr
          35             40             45

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ttt tat agg agc agt ttt caa ctc cta aat gtt gaa tat aat agt cag      253
Phe Tyr Arg Ser Ser Phe Gln Leu Leu Asn Val Glu Tyr Asn Ser Gln
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tta aat tca cca gct aca cag gaa tac agg act ttg agt gga aga att      301
Leu Asn Ser Pro Ala Thr Gln Glu Tyr Arg Thr Leu Ser Gly Arg Ile
          65             70             75             80

```

```

gaa tct ctg att act aaa aca ttc aaa gaa tca aat tta aga aat cag      349
Glu Ser Leu Ile Thr Lys Thr Phe Lys Glu Ser Asn Leu Arg Asn Gln
          85             90             95

```

```

ttc atc aga gct cat gtt gcc aaa ctg agg caa gat ggt agt ggt gtg      397
Phe Ile Arg Ala His Val Ala Lys Leu Arg Gln Asp Gly Ser Gly Val
          100             105             110

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aga gcg gat gtt gtc atg aaa ttt caa ttc act aga aat aac aat gga      445
Arg Ala Asp Val Val Met Lys Phe Gln Phe Thr Arg Asn Asn Asn Gly
          115             120             125

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```

gca tca atg aaa agc aga att gag tct gtt tta cga caa atg ctg aat      493
Ala Ser Met Lys Ser Arg Ile Glu Ser Val Leu Arg Gln Met Leu Asn
          130             135             140

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aac tct gga aac ctg gaa ata aac cct tca act gag ata aca tca ctt      541
Asn Ser Gly Asn Leu Glu Ile Asn Pro Ser Thr Glu Ile Thr Ser Leu
          145             150             155             160

```

```

act gac cag gct gca gca aat tgg ctt att aat gaa tgt ggg gcc ggt      589
Thr Asp Gln Ala Ala Ala Asn Trp Leu Ile Asn Glu Cys Gly Ala Gly
          165             170             175

```

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cca gac cta ata aca ttg tct gag cag aga atc ctt gga ggc act gag      637
Pro Asp Leu Ile Thr Leu Ser Glu Gln Arg Ile Leu Gly Gly Thr Glu
          180             185             190

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gct gag gag gga agc tgg ccg tgg caa gtc agt ctg cgg ctc aat aat	685
Ala Glu Glu Gly Ser Trp Pro Trp Gln Val Ser Leu Arg Leu Asn Asn	
195 200 205	
gcc cac cac tgt gga ggc agc ctg atc aat aac atg tgg atc ctg aca	733
Ala His His Cys Gly Gly Ser Leu Ile Asn Asn Met Trp Ile Leu Thr	
210 215 220	
gca gct cac tgc ttc aga agc aac tct aat cct cgt gac tgg att gcc	781
Ala Ala His Cys Phe Arg Ser Asn Ser Asn Pro Arg Asp Trp Ile Ala	
225 230 235 240	
acg tct ggt att toc aca aca ttt cct aaa cta aga atg aga gta aga	829
Thr Ser Gly Ile Ser Thr Thr Phe Pro Lys Leu Arg Met Arg Val Arg	
245 250 255	
aat att tta att cat aac aat tat aaa tct gca act cat gaa aat gac	877
Asn Ile Leu Ile His Asn Asn Tyr Lys Ser Ala Thr His Glu Asn Asp	
260 265 270	
att gca ctt gtg aga ctt gag aac agt gtc acc ttt acc aaa gat atc	925
Ile Ala Leu Val Arg Leu Glu Asn Ser Val Thr Phe Thr Lys Asp Ile	
275 280 285	
cat agt gtg tgt ctc cca gct gct acc cag aat att cca cct ggc tct	973
His Ser Val Cys Leu Pro Ala Ala Thr Gln Asn Ile Pro Pro Gly Ser	
290 295 300	
act gct tat gta aca gga tgg ggc gct caa gaa tat gct ggc cac aca	1021
Thr Ala Tyr Val Thr Gly Trp Gly Ala Gln Glu Tyr Ala Gly His Thr	
305 310 315 320	
gtt cca gag cta agg caa gga cag gtc aga ata ata agt aat gat gta	1069
Val Pro Glu Leu Arg Gln Gly Gln Val Arg Ile Ile Ser Asn Asp Val	
325 330 335	
tgt aat gca cca cat agt tat aat gga gcc atc ttg tct gga atg ctg	1117
Cys Asn Ala Pro His Ser Tyr Asn Gly Ala Ile Leu Ser Gly Met Leu	
340 345 350	
tgt gct gga gta cct caa ggt gga gtg gac gca tgt cag ggt gac tct	1165
Cys Ala Gly Val Pro Gln Gly Gly Val Asp Ala Cys Gln Gly Asp Ser	
355 360 365	
ggt ggc cca cta gta caa gaa gac tca cgg cgg ctt tgg ttt att gtg	1213
Gly Gly Pro Leu Val Gln Glu Asp Ser Arg Arg Leu Trp Phe Ile Val	
370 375 380	
ggg ata gta agc tgg gga gat cag tgt ggc ctg ccg gat aag cca gga	1261
Gly Ile Val Ser Trp Gly Asp Gln Cys Gly Leu Pro Asp Lys Pro Gly	
385 390 395 400	
gtg tat act cga gtg aca gcc tac ctt gac tgg att agg caa caa act	1309
Val Tyr Thr Arg Val Thr Ala Tyr Leu Asp Trp Ile Arg Gln Gln Thr	
405 410 415	
ggg atc tag tgcaacaagt gcatccctgt tgcaaagtct gtatgcaggt	1358
Gly Ile *	

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```

gtgcctgtct taaattccaa agctttacat ttcaactgaa aaagaaacta gaaatgtcct 1418
aatttaacat cttgttacat aaatatggtt taacaaacac tgtttaacct ttctttatta 1478
ttaaagggtt tctattttct cc 1500

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<210> 33
<211> 418
<212> PRT
<213> Homo Sapien

```

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<400> 33
Met Tyr Arg Pro Ala Arg Val Thr Ser Thr Ser Arg Phe Leu Asn Pro
1      5      10      15
Tyr Val Val Cys Phe Ile Val Val Ala Gly Val Val Ile Leu Ala Val
20     25     30
Thr Ile Ala Leu Leu Val Tyr Phe Leu Ala Phe Asp Gln Lys Ser Tyr
35     40     45
Phe Tyr Arg Ser Ser Phe Gln Leu Leu Asn Val Glu Tyr Asn Ser Gln
50     55     60
Leu Asn Ser Pro Ala Thr Gln Glu Tyr Arg Thr Leu Ser Gly Arg Ile
65     70     75     80
Glu Ser Leu Ile Thr Lys Thr Phe Lys Glu Ser Asn Leu Arg Asn Gln
85     90     95
Phe Ile Arg Ala His Val Ala Lys Leu Arg Gln Asp Gly Ser Gly Val
100    105    110
Arg Ala Asp Val Val Met Lys Phe Gln Phe Thr Arg Asn Asn Asn Gly
115    120    125
Ala Ser Met Lys Ser Arg Ile Glu Ser Val Leu Arg Gln Met Leu Asn
130    135    140
Asn Ser Gly Asn Leu Glu Ile Asn Pro Ser Thr Glu Ile Thr Ser Leu
145    150    155    160
Thr Asp Gln Ala Ala Asn Trp Leu Ile Asn Glu Cys Gly Ala Gly
165    170    175
Pro Asp Leu Ile Thr Leu Ser Glu Gln Arg Ile Leu Gly Gly Thr Glu
180    185    190
Ala Glu Glu Gly Ser Trp Pro Trp Gln Val Ser Leu Arg Leu Asn Asn
195    200    205
Ala His His Cys Gly Gly Ser Leu Ile Asn Asn Met Trp Ile Leu Thr
210    215    220
Ala Ala His Cys Phe Arg Ser Asn Ser Asn Pro Arg Asp Trp Ile Ala
225    230    235    240
Thr Ser Gly Ile Ser Thr Thr Phe Pro Lys Leu Arg Met Arg Val Arg
245    250    255
Asn Ile Leu Ile His Asn Asn Tyr Lys Ser Ala Thr His Glu Asn Asp
260    265    270
Ile Ala Leu Val Arg Leu Glu Asn Ser Val Thr Phe Thr Lys Asp Ile
275    280    285
His Ser Val Cys Leu Pro Ala Ala Thr Gln Asn Ile Pro Pro Gly Ser
290    295    300
Thr Ala Tyr Val Thr Gly Trp Gly Ala Gln Glu Tyr Ala Gly His Thr
305    310    315    320
Val Pro Glu Leu Arg Gln Gly Gln Val Arg Ile Ile Ser Asn Asp Val
325    330    335
Cys Asn Ala Pro His Ser Tyr Asn Gly Ala Ile Leu Ser Gly Met Leu
340    345    350
Cys Ala Gly Val Pro Gln Gly Gly Val Asp Ala Cys Gln Gly Asp Ser
355    360    365
Gly Gly Pro Leu Val Gln Glu Asp Ser Arg Arg Leu Trp Phe Ile Val
370    375    380
Gly Ile Val Ser Trp Gly Asp Gln Cys Gly Leu Pro Asp Lys Pro Gly
385    390    395    400
Val Tyr Thr Arg Val Thr Ala Tyr Leu Asp Trp Ile Arg Gln Gln Thr

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Gly Ile 405 410 415

<210> 34
 <211> 1783
 <212> DNA
 <213> Homo Sapien

<220>
 <221> CDS
 <222> (246)...(1499)
 <223> Nucleic acid encoding human hepsin

<300>
 <308> GenBank M18930
 <309> 1993-06-11

<400> 34
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 agggcccccag ccaccgcctc tgcctccagg ccgcccgcctg ctgcgggggcc accatgctcc 120
 tgcccaggcc tggagactga cccgaccccg gcaactacctc gaggtccgc cccacactgc 180
 tggaccccgag ggtcccaccc tggcccaggga ggtagccagc ggaatcatta acaagaggca 240
 gtgac atg gcg cag aag gag ggt ggc cgg act gtg cca tgc tgc tcc aga 290
 Met Ala Gln Lys Glu Gly Gly Arg Thr Val Pro Cys Cys Ser Arg
 1 5 10 15

ccc aag gtg gca gct ctc act gcg ggg acc ctg cta ctt ctg aca gcc 338
 Pro Lys Val Ala Ala Leu Thr Ala Gly Thr Leu Leu Leu Leu Thr Ala
 20 25 30

atc ggg gcg gca tcc tgg gcc att gtg gct gtt ctc ctc agg agt gac 386
 Ile Gly Ala Ala Ser Trp Ala Ile Val Ala Val Leu Leu Arg Ser Asp
 35 40 45

cag gag ccg ctg tac cca gtg cag gtc agc tct gcg gac gct cgg ctc 434
 Gln Glu Pro Leu Tyr Pro Val Gln Val Ser Ser Ala Asp Ala Arg Leu
 50 55 60

atg gtc ttt gac aag acg gaa ggg acg tgg cgg ctg ctg tgc tcc tcg 482
 Met Val Phe Asp Lys Thr Glu Gly Thr Trp Arg Leu Leu Cys Ser Ser
 65 70 75

cgc tcc aac gcc agg gta gcc gga ctc agc tgc gag gag atg ggc ttc 530
 Arg Ser Asn Ala Arg Val Ala Gly Leu Ser Cys Glu Glu Met Gly Phe
 80 85 90 95

ctc agg gca ctg acc cac tcc gag ctg gac gtg cga acg gcg ggc gcc 578
 Leu Arg Ala Leu Thr His Ser Glu Leu Asp Val Arg Thr Ala Gly Ala
 100 105 110

aat ggc acg tcg ggc ttc ttc tgt gtg gac gag ggg agg ctg ccc cac 626
 Asn Gly Thr Ser Gly Phe Phe Cys Val Asp Glu Gly Arg Leu Pro His
 115 120 125

acc cag agg ctg ctg gag gtc atc tcc gtg tgt gat tgc ccc aga ggc 674
 Thr Gln Arg Leu Leu Glu Val Ile Ser Val Cys Asp Cys Pro Arg Gly
 130 135 140

cgt ttc ttg gcc gcc atc tgc caa gac tgt ggc cgc agg aag ctg ccc 722
 Arg Phe Leu Ala Ala Ile Cys Gln Asp Cys Gly Arg Arg Lys Leu Pro
 145 150 155

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gtg gac cgc atc gtg gga ggc cgg gac acc agc ttg ggc cgg tgg ccg Val Asp Arg Ile Val Gly Gly Arg Asp Thr Ser Leu Gly Arg Trp Pro 160 165 170 175	770
tgg caa gtc agc ctt cgc tat gat gga gca cac ctc tgt ggg gga tcc Trp Gln Val Ser Leu Arg Tyr Asp Gly Ala His Leu Cys Gly Gly Ser 180 185 190	818
ctg ctc tcc ggg gac tgg gtg ctg aca gcc gcc cac tgc ttc ccg gag Leu Leu Ser Gly Asp Trp Val Leu Thr Ala Ala His Cys Phe Pro Glu 195 200 205	866
cgg aac cgg gtc ctg tcc cga tgg cga gtg ttt gcc ggt gcc gtg gcc Arg Asn Arg Val Leu Ser Arg Trp Arg Val Phe Ala Gly Ala Val Ala 210 215 220	914
cag gcc tct ccc cac ggt ctg cag ctg ggg gtg cag gct gtg gtc tac Gln Ala Ser Pro His Gly Leu Gln Leu Gly Val Gln Ala Val Val Tyr 225 230 235	962
cac ggg ggc tat ctt ccc ttt cgg gac ccc aac agc gag gag aac agc His Gly Gly Tyr Leu Pro Phe Arg Asp Pro Asn Ser Glu Glu Asn Ser 240 245 250 255	1010
aac gat att gcc ctg gtc cac ctc tcc agt ccc ctg ccc ctc aca gaa Asn Asp Ile Ala Leu Val His Leu Ser Ser Pro Leu Pro Leu Thr Glu 260 265 270	1058
tac atc cag cct gtg tgc ctc cca gct gcc ggc cag gcc ctg gtg gat Tyr Ile Gln Pro Val Cys Leu Pro Ala Ala Gly Gln Ala Leu Val Asp 275 280 285	1106
ggc aag atc tgt acc gtg acg ggc tgg ggc aac acg cag tac tat ggc Gly Lys Ile Cys Thr Val Thr Gly Trp Gly Asn Thr Gln Tyr Tyr Gly 290 295 300	1154
caa cag gcc ggg gta ctc cag gag gct cga gtc ccc ata atc agc aat Gln Gln Ala Gly Val Leu Gln Glu Ala Arg Val Pro Ile Ile Ser Asn 305 310 315	1202
gat gtc tgc aat ggc gct gac ttc tat gga aac cag atc aag ccc aag Asp Val Cys Asn Gly Ala Asp Phe Tyr Gly Asn Gln Ile Lys Pro Lys 320 325 330 335	1250
atg ttc tgt gct ggc tac ccc gag ggt ggc att gat gcc tgc cag ggc Met Phe Cys Ala Gly Tyr Pro Glu Gly Gly Ile Asp Ala Cys Gln Gly 340 345 350	1298
gac agc ggt ggt ccc ttt gtg tgt gag gac agc atc tct cgg acg cca Asp Ser Gly Gly Pro Phe Val Cys Glu Asp Ser Ile Ser Arg Thr Pro 355 360 365	1346
cgt tgg cgg ctg tgt ggc att gtg agt tgg ggc act ggc tgt gcc ctg Arg Trp Arg Leu Cys Gly Ile Val Ser Trp Gly Thr Gly Cys Ala Leu 370 375 380	1394
gcc cag aag cca ggc gtc tac acc aaa gtc agt gac ttc cgg gag tgg Ala Gln Lys Pro Gly Val Tyr Thr Lys Val Ser Asp Phe Arg Glu Trp 385 390 395	1442

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atc ttc cag gcc ata aag act cac tcc gaa gcc agc ggc atg gtg acc 1490
 ile phe gln ala ile lys thr his ser glu ala ser gly met val thr
 400 405 410 415

cag ctc tga ccgggtggctt ctgctgctgcgc agcctccagg gcccgaggtg 1539
 gln leu *

atcccggtgg tgggatccac gctggggccga ggatgggacg tttttcttct tgggccccgt 1599
 ccacaggtcc aaggacaccc tccctccagg gtcctctctt ccacagtggc gggcccactc 1659
 agccccgaga ccacccaacc tcacctctct gacccccatg taaatattgt tctgctgtct 1719
 gggactcctg tctaggtgcc cctgatgatg ggatgctctt taaataataa agatgggtttt 1779
 gatt 1783

<210> 35
 <211> 417
 <212> PRT
 <213> Homo Sapien

<400> 35
 Met Ala Gln Lys Glu Gly Gly Arg Thr Val Pro Cys Cys Ser Arg Pro
 1 5 10 15
 Lys Val Ala Ala Leu Thr Ala Gly Thr Leu Leu Leu Leu Thr Ala Ile
 20 25 30
 Gly Ala Ala Ser Trp Ala Ile Val Ala Val Leu Leu Arg Ser Asp Gln
 35 40 45
 Glu Pro Leu Tyr Pro Val Gln Val Ser Ser Ala Asp Ala Arg Leu Met
 50 55 60
 Val Phe Asp Lys Thr Glu Gly Thr Trp Arg Leu Leu Cys Ser Ser Arg
 65 70 75 80
 Ser Asn Ala Arg Val Ala Gly Leu Ser Cys Glu Glu Met Gly Phe Leu
 85 90 95
 Arg Ala Leu Thr His Ser Glu Leu Asp Val Arg Thr Ala Gly Ala Asn
 100 105 110
 Gly Thr Ser Gly Phe Phe Cys Val Asp Glu Gly Arg Leu Pro His Thr
 115 120 125
 Gln Arg Leu Leu Glu Val Ile Ser Val Cys Asp Cys Pro Arg Gly Arg
 130 135 140
 Phe Leu Ala Ala Ile Cys Gln Asp Cys Gly Arg Arg Lys Leu Pro Val
 145 150 155 160
 Asp Arg Ile Val Gly Gly Arg Asp Thr Ser Leu Gly Arg Trp Pro Trp
 165 170 175
 Gln Val Ser Leu Arg Tyr Asp Gly Ala His Leu Cys Gly Gly Ser Leu
 180 185 190
 Leu Ser Gly Asp Trp Val Leu Thr Ala Ala His Cys Phe Pro Glu Arg
 195 200 205
 Asn Arg Val Leu Ser Arg Trp Arg Val Phe Ala Gly Ala Val Ala Gln
 210 215 220
 Ala Ser Pro His Gly Leu Gln Leu Gly Val Gln Ala Val Val Tyr His
 225 230 235 240
 Gly Gly Tyr Leu Pro Phe Arg Asp Pro Asn Ser Glu Glu Asn Ser Asn
 245 250 255
 Asp Ile Ala Leu Val His Leu Ser Ser Pro Leu Pro Leu Thr Glu Tyr
 260 265 270
 Ile Gln Pro Val Cys Leu Pro Ala Ala Gly Gln Ala Leu Val Asp Gly
 275 280 285
 Lys Ile Cys Thr Val Thr Gly Trp Gly Asn Thr Gln Tyr Tyr Gly Gln
 290 295 300
 Gln Ala Gly Val Leu Gln Glu Ala Arg Val Pro Ile Ile Ser Asn Asp
 305 310 315 320
 Val Cys Asn Gly Ala Asp Phe Tyr Gly Asn Gln Ile Lys Pro Lys Met

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```

          325          330          335
Phe Cys Ala Gly Tyr Pro Glu Gly Gly Ile Asp Ala Cys Gln Gly Asp
          340          345          350
Ser Gly Gly Pro Phe Val Cys Glu Asp Ser Ile Ser Arg Thr Pro Arg
          355          360          365
Trp Arg Leu Cys Gly Ile Val Ser Trp Gly Thr Gly Cys Ala Leu Ala
          370          375          380
Gln Lys Pro Gly Val Tyr Thr Lys Val Ser Asp Phe Arg Glu Trp Ile
          385          390          395          400
Phe Gln Ala Ile Lys Thr His Ser Glu Ala Ser Gly Met Val Thr Gln
          405          410          415
Leu

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<210> 36

<211> 2479

<212> DNA

<213> Homo sapien

<220>

<221> CDS

<222> (57) ... (1535)

<223> Nucleotide sequence encoding human serine protease (TMPRSS2)

<300>

<308> GenBank U75329

<309> 1997-10-10

<400> 36

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gtcatattga acattccaga tacctatcat tactogatgc tgttgataac agcaag atg      59
                                     Met
                                     1

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gct ttg aac tca ggg tca cca cca gct att gga cct tac tat gaa aac      107
Ala Leu Asn Ser Gly Ser Pro Pro Ala Ile Gly Pro Tyr Tyr Glu Asn
          5          10          15

```

```

cat gga tac caa ccg gaa aac ccc tat ccc gca cag ccc act gtg gtc      155
His Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val Val
          20          25          30

```

```

ccc act gtc tac gag gtg cat ccg gct cag tac tac ccg tcc ccc gtg      203
Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro Val
          35          40          45

```

```

ccc cag tac gcc ccg agg gtc ctg acg cag gct tcc aac ccc gtc gtc      251
Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val Val
          50          55          60          65

```

```

tgc acg cag ccc aaa tcc cca tcc ggg aca gtg tgc acc tca aag act      299
Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys Thr
          70          75          80

```

```

aag aaa gca ctg tgc atc acc ttg acc ctg ggg acc ttc ctc gtg gga      347
Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val Gly
          85          90          95

```

```

gct gcg ctg gcc gct ggc cta ctc tgg aag ttc atg ggc agc aag tgc      395
Ala Ala Leu Ala Ala Gly Leu Trp Lys Phe Met Gly Ser Lys Cys
          100          105          110

```

```

tcc aac tct ggg ata gag tgc gac tcc tca ggt acc tgc atc aac ccc      443

```

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Ser	Asn	Ser	Gly	Ile	Glu	Cys	Asp	Ser	Ser	Gly	Thr	Cys	Ile	Asn	Pro	
115						120					125					
tct	aac	tgg	tgt	gat	ggc	gtg	tca	cac	tgc	ccc	ggc	ggg	gag	gac	gag	491
Ser	Asn	Trp	Cys	Asp	Gly	Val	Ser	His	Cys	Pro	Gly	Gly	Glu	Asp	Glu	
130					135					140					145	
aat	cgg	tgt	gtt	cgc	ctc	tac	gga	cca	aac	ttc	atc	ctt	cag	atg	tac	539
Asn	Arg	Cys	Val	Arg	Leu	Tyr	Gly	Pro	Asn	Phe	Ile	Leu	Gln	Met	Tyr	
			150						155					160		
tca	tct	cag	agg	aag	tcc	tgg	cac	cct	gtg	tgc	caa	gac	gac	tgg	aac	587
Ser	Ser	Gln	Arg	Lys	Ser	Trp	His	Pro	Val	Cys	Gln	Asp	Asp	Trp	Asn	
			165					170					175			
gag	aac	tac	ggg	cgg	gcg	gcc	tgc	agg	gac	atg	ggc	tat	aag	aat	aat	635
Glu	Asn	Tyr	Gly	Arg	Ala	Ala	Cys	Arg	Asp	Met	Gly	Tyr	Lys	Asn	Asn	
		180					185					190				
ttt	tac	tct	agc	caa	gga	ata	gtg	gat	gac	agc	gga	tcc	acc	agc	ttt	683
Phe	Tyr	Ser	Ser	Gln	Gly	Ile	Val	Asp	Asp	Ser	Gly	Ser	Thr	Ser	Phe	
	195					200					205					
atg	aaa	ctg	aac	aca	agt	gcc	ggc	aat	gtc	gat	atc	tat	aaa	aaa	ctg	731
Met	Lys	Leu	Asn	Thr	Ser	Ala	Gly	Asn	Val	Asp	Ile	Tyr	Lys	Lys	Leu	
210					215					220					225	
tac	cac	agt	gat	gcc	tgt	tct	tca	aaa	gca	gtg	gtt	tct	tta	cgc	tgt	779
Tyr	His	Ser	Asp	Ala	Cys	Ser	Ser	Lys	Ala	Val	Val	Ser	Leu	Arg	Cys	
				230					235					240		
tta	gcc	tgc	ggg	gtc	aac	ttg	aac	tca	agc	cgc	cag	agc	agg	atc	gtg	827
Leu	Ala	Cys	Gly	Val	Asn	Leu	Asn	Ser	Ser	Arg	Gln	Ser	Arg	Ile	Val	
			245				250						255			
ggc	ggt	gag	agc	gcg	ctc	ccg	ggg	gcc	tgg	ccc	tgg	cag	gtc	agc	ctg	875
Gly	Gly	Glu	Ser	Ala	Leu	Pro	Gly	Ala	Trp	Pro	Trp	Gln	Val	Ser	Leu	
		260					265					270				
cac	gtc	cag	aac	gtc	cac	gtg	tgc	gga	ggc	tcc	atc	atc	acc	ccc	gag	923
His	Val	Gln	Asn	Val	His	Val	Cys	Gly	Gly	Ser	Ile	Ile	Thr	Pro	Glu	
		275				280					285					
tgg	atc	gtg	aca	gcc	gcc	cac	tgc	gtg	gaa	aaa	cct	ctt	aac	aat	cca	971
Trp	Ile	Val	Thr	Ala	Ala	His	Cys	Val	Glu	Lys	Pro	Leu	Asn	Asn	Pro	
290					295				300						305	
tgg	cat	tgg	acg	gca	ttt	gcg	ggg	att	ttg	aga	caa	tct	ttc	atg	ttc	1019
Trp	His	Trp	Thr	Ala	Phe	Ala	Gly	Ile	Leu	Arg	Gln	Ser	Phe	Met	Phe	
				310				315						320		
tat	gga	gcc	gga	tac	caa	gta	caa	aaa	gtg	att	tct	cat	cca	aat	tat	1067
Tyr	Gly	Ala	Gly	Tyr	Gln	Val	Gln	Lys	Val	Ile	Ser	His	Pro	Asn	Tyr	
			325				330						335			
gac	tcc	aag	acc	aag	aac	aat	gac	att	gcg	ctg	atg	aag	ctg	cag	aag	1115
Asp	Ser	Lys	Thr	Lys	Asn	Asn	Asp	Ile	Ala	Leu	Met	Lys	Leu	Gln	Lys	
		340					345					350				
cct	ctg	act	ttc	aac	gac	cta	gtg	aaa	cca	gtg	tgt	ctg	ccc	aac	cca	1163
Pro	Leu	Thr	Phe	Asn	Asp	Leu	Val	Lys	Pro	Val	Cys	Leu	Pro	Asn	Pro	

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355	360	365	
ggc atg atg ctg cag cca gaa cag ctc tgc tgg att tcc ggg tgg ggg			1211
Gly Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp Gly			
370	375	380	385
gcc acc gag gag aaa ggg aag acc tca gaa gtg ctg aac gct gcc aag			1259
Ala Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala Lys			
	390	395	400
gtg ctt ctc att gag aca cag aga tgc aac agc aga tat gtc tat gac			1307
Val Leu Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr Asp			
	405	410	415
aac ctg atc aca cca gcc atg atc tgt gcc ggc ttc ctg cag ggg aac			1355
Asn Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly Asn			
	420	425	430
gtc gat tct tgc cag ggt gac agt gga ggg cct ctg gtc act tog aac			1403
Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser Asn			
	435	440	445
aac aat atc tgg tgg ctg ata ggg gat aca agc tgg ggt tct ggc tgt			1451
Asn Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly Cys			
	450	455	460
gcc aaa gct tac aga cca gga gtg tac ggg aat gtg atg gta ttc acg			1499
Ala Lys Ala Tyr Arg Pro Gly Val Tyr Gly Asn Val Met Val Phe Thr			
	470	475	480
gac tgg att tat cga caa atg aag gca aac ggc taa tccacatggt			1545
Asp Trp Ile Tyr Arg Gln Met Lys Ala Asn Gly *			
	485	490	

cttcgtcctt gacgtcgttt tacaagaaaa caatggggct ggttttgctt cccogtgcat 1605
 gatttactct tagagatgat tcagaggtca cttcattttt attaaacagt gaacttgtct 1665
 ggcttttgca ctctctgcca tactgtgcag gctgcagtgg ctccctgcc cagcctgctc 1725
 tccctaacc cttgtccgca aggggtgatg gccggctggt tgtgggcaact ggcgggtcaat 1785
 tgtggaagga agagggttgg aggcctgcccc cattgagatc ttccctgctga gtcctttcca 1845
 ggggcccaatt ttggatgagc atggagctgt cacttctcag ctgctggatg acttgagatg 1905
 aaaaaggaga gacatggaaa gggagacagc cagggtggcac ctgcagcggc tgcctctggt 1965
 ggccacttgg tagtgtcccc agcctacttc acaaggggat tttgctgatg ggttcttaga 2025
 gccttagcag ccctggatgg tggccagaaa taaagggacc agcccttcat ggggtggtgac 2085
 gtggtagtca cttgtaaggg gaacagaaac atttttgctt ttatggggtg agaatataga 2145
 cagtgccttt ggtgcgaggg aagcaattga aaaggaactt gccctgagca ctccctggtgc 2205
 aggtctccac ctgcacattg ggtggggctc ctgggaggga gactcagcct tcctcctcat 2265
 cctccctgac cctgctccta gcaccctgga gactgaatgc cccttgggtcc ctggcagggc 2325
 gccaaagtgt gcaccatgtc ggcctcttca ggctgatag tcattggaaa ttgaggtcca 2385
 tgggggaaat caaggatgct cagttaagg tacactgttt ccatgttatg tttctacaca 2445
 ttgatggtgg tgaccctgag ttcaaagcca tctt 2479

<210> 37

<211> 492

<212> PRT

<213> Homo sapien

<400> 37

Met	Ala	Leu	Asn	Ser	Gly	Ser	Pro	Pro	Ala	Ile	Gly	Pro	Tyr	Tyr	Glu
1				5				10					15		
Asn	His	Gly	Tyr	Gln	Pro	Glu	Asn	Pro	Tyr	Pro	Ala	Gln	Pro	Thr	Val
		20					25					30			

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Val Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro
 35 40 45
 Val Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val
 50 55 60
 Val Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys
 65 70 75 80
 Thr Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val
 85 90 95
 Gly Ala Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys
 100 105 110
 Cys Ser Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn
 115 120 125
 Pro Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp
 130 135 140
 Glu Asn Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Met
 145 150 155 160
 Tyr Ser Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp
 165 170 175
 Asn Glu Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn
 180 185 190
 Asn Phe Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser
 195 200 205
 Phe Met Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys
 210 215 220
 Leu Tyr His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg
 225 230 235 240
 Cys Leu Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile
 245 250 255
 Val Gly Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser
 260 265 270
 Leu His Val Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro
 275 280 285
 Glu Trp Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn
 290 295 300
 Pro Trp His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met
 305 310 315 320
 Phe Tyr Gly Ala Gly Tyr Gln Val Gln Lys Val Ile Ser His Pro Asn
 325 330 335
 Tyr Asp Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln
 340 345 350
 Lys Pro Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn
 355 360 365
 Pro Gly Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp
 370 375 380
 Gly Ala Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala
 385 390 395 400
 Lys Val Leu Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr
 405 410 415
 Asp Asn Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly
 420 425 430
 Asn Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser
 435 440 445
 Asn Asn Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly
 450 455 460
 Cys Ala Lys Ala Tyr Arg Pro Gly Val Tyr Gly Asn Val Met Val Phe
 465 470 475 480
 Thr Asp Trp Ile Tyr Arg Gln Met Lys Ala Asn Gly
 485 490

<210> 38
 <211> 2079

-77-

<212> DNA
 <213> Homo sapien

<220>
 <221> CDS
 <222> (251)...(1522)
 <223> Nucleotide sequence encoding transmembrane
 protease, serine 4 (TMPRSS4)

<300>
 <308> GenBank NM016425
 <309> 2000-11-06

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 gacctgtgtg gggaggccct cctgtgtgct tggggtgaca atctcagctc caggctacag 180
 ggagaccggg aggatcacag agccagcatg gtacaggatc ctgacagtga tcaacctctg 240
 aacagcctcg atg tca aac ccc tgc gca aac ccc gta tcc cca tgg aga 289
 Met Ser Asn Pro Cys Ala Asn Pro Val Ser Pro Trp Arg
 1 5 10
 cct tca gaa agt gtg ggg atc ccc atc atc ata gca cta ctg agc ctg 337
 Pro Ser Glu Ser Val Gly Ile Pro Ile Ile Ile Ala Leu Leu Ser Leu
 15 20 25
 gcg agt atc atc att gtg gtt gtc ctc atc aag gtg att ctg gat aaa 385
 Ala Ser Ile Ile Ile Val Val Leu Ile Lys Val Ile Leu Asp Lys
 30 35 40 45
 tac tac ttc ctc tgc ggg cag cct ctc cac ttc atc ccg agg aag cag 433
 Tyr Tyr Phe Leu Cys Gly Gln Pro Leu His Phe Ile Pro Arg Lys Gln
 50 55 60
 ctg tgt gac gga gag ctg gac tgt ccc ttg ggg gag gac gag gag cac 481
 Leu Cys Asp Gly Glu Leu Asp Cys Pro Leu Gly Glu Asp Glu Glu His
 65 70 75
 tgt gtc aag agc ttc ccc gaa ggg cct gca gtg gca gtc cgc ctc tcc 529
 Cys Val Lys Ser Phe Pro Glu Gly Pro Ala Val Ala Val Arg Leu Ser
 80 85 90
 aag gac cga tcc aca ctg cag gtg ctg gac tcg gcc aca ggg aac tgg 577
 Lys Asp Arg Ser Thr Leu Gln Val Leu Asp Ser Ala Thr Gly Asn Trp
 95 100 105
 ttc tct gcc tgt ttc gac aac ttc aca gaa gct ctc gct gag aca gcc 625
 Phe Ser Ala Cys Phe Asp Asn Phe Thr Glu Ala Leu Ala Glu Thr Ala
 110 115 120 125
 tgt agg cag atg ggc tac agc agc aaa ccc act ttc aga gct gtg gag 673
 Cys Arg Gln Met Gly Tyr Ser Ser Lys Pro Thr Phe Arg Ala Val Glu
 130 135 140
 att ggc cca gac cag gat ctg gat gtt gtt gaa atc aca gaa aac agc 721
 Ile Gly Pro Asp Gln Asp Leu Asp Val Val Glu Ile Thr Glu Asn Ser
 145 150 155
 cag gag ctt cgc atg cgg aac tca agt ggg ccc tgt ctc tca ggc tcc 769
 Gln Glu Leu Arg Met Arg Asn Ser Ser Gly Pro Cys Leu Ser Gly Ser
 160 165 170

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ctg gtc tcc ctg cac tgt ctt gcc tgt ggg aag agc ctg aag acc ccc Leu Val Ser Leu His Cys Leu Ala Cys Gly Lys Ser Leu Lys Thr Pro 175 180 185	817
cgt gtg gtg ggt ggg gag gag gcc tct gtg gat tct tgg cct tgg cag Arg Val Val Gly Gly Glu Glu Ala Ser Val Asp Ser Trp Pro Trp Gln 190 195 200 205	865
gtc agc atc cag tac gac aaa cag cac gtc tgt gga ggg agc atc ctg Val Ser Ile Gln Tyr Asp Lys Gln His Val Cys Gly Gly Ser Ile Leu 210 215 220	913
gac ccc cac tgg gtc ctc acg gca gcc cac tgc ttc agg aaa cat acc Asp Pro His Trp Val Leu Thr Ala Ala His Cys Phe Arg Lys His Thr 225 230 235	961
gat gtg ttc aac tgg aag gtg cgg gca ggc tca gac aaa ctg ggc agc Asp Val Phe Asn Trp Lys Val Arg Ala Gly Ser Asp Lys Leu Gly Ser 240 245 250	1009
ttc cca tcc ctg gct gtg gcc aag atc atc atc att gaa ttc aac ccc Phe Pro Ser Leu Ala Val Ala Lys Ile Ile Ile Ile Glu Phe Asn Pro 255 260 265	1057
atg tac ccc aaa gac aat gac atc gcc ctc atg aag ctg cag ttc cca Met Tyr Pro Lys Asp Asn Asp Ile Ala Leu Met Lys Leu Gln Phe Pro 270 275 280 285	1105
ctc act ttc tca ggc aca gtc agg ccc atc tgt ctg ccc ttc ttt gat Leu Thr Phe Ser Gly Thr Val Arg Pro Ile Cys Leu Pro Phe Phe Asp 290 295 300	1153
gag gag ctc act cca gcc acc cca ctc tgg atc att gga tgg ggc ttt Glu Glu Leu Thr Pro Ala Thr Pro Leu Trp Ile Ile Gly Trp Gly Phe 305 310 315	1201
acg aag cag aat gga ggg aag atg tct gac ata ctg ctg cag gcg tca Thr Lys Gln Asn Gly Gly Lys Met Ser Asp Ile Leu Leu Gln Ala Ser 320 325 330	1249
gtc cag gtc att gac agc aca cgg tgc aat gca gac gat gcg tac cag Val Gln Val Ile Asp Ser Thr Arg Cys Asn Ala Asp Asp Ala Tyr Gln 335 340 345	1297
ggg gaa gtc acc gag aag atg atg tgt gca ggc atc ccg gaa ggg ggt Gly Glu Val Thr Glu Lys Met Met Cys Ala Gly Ile Pro Glu Gly Gly 350 355 360 365	1345
gtg gac acc tgc cag ggt gac agt ggt ggg ccc ctg atg tac caa tct Val Asp Thr Cys Gln Gly Asp Ser Gly Gly Pro Leu Met Tyr Gln Ser 370 375 380	1393
gac cag tgg cat gtg gtg ggc atc gtt agc tgg ggc tat ggc tgc ggg Asp Gln Trp His Val Val Gly Ile Val Ser Trp Gly Tyr Gly Cys Gly 385 390 395	1441
ggc ccg agc acc cca gga gta tac acc aag gtc tca gcc tat ctc aac Gly Pro Ser Thr Pro Gly Val Tyr Thr Lys Val Ser Ala Tyr Leu Asn 400 405 410	1489

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tgg atc tac aat gtc tgg aag gct gag ctg taa tgctgctgcc cctttgcagt 1542
 Trp Ile Tyr Asn Val Trp Lys Ala Glu Leu *
 415 420

gctggggagcc gcttccttcc tgccttgccc acctgggggat ccccaaaagt cagacacaga 1602
 gcaagagtc ccttgggtac acccctctgc ccacagcctc agcatttctt ggagcagcaa 1662
 agggcctcaa ttctgtgaag agaccctcgc agcccagagg cgcccagagg aagtcagcag 1722
 ccctagctcg gccacacttg gtgctcccag catcccaggg agagacacag cccactgaac 1782
 aaggtctcag gggatttgct aagccaagaa ggaactttcc cacactactg aatggaagca 1842
 ggctgtcttg taaaagccca gatcactgtg ggctggagag gagaaggaaa gggctctgcgc 1902
 cagccctgtc cgtcttcacc catccccaag cctactagag caagaaacca gttgtaatat 1962
 aaaatgcact gccctactgt tggatgact accgttacct actgttgtca ttgttattac 2022
 agctatggcc actattatta aagagctgtg taacatcaaa aaaaaaaaaa aaaaaaa 2079

<210> 39
 <211> 423
 <212> PRT
 <213> Homo sapien

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 Ser Val Gly Ile Pro Ile Ile Ile Ala Leu Leu Ser Leu Ala Ser Ile
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 Ile Ile Val Val Val Leu Ile Lys Val Ile Leu Asp Lys Tyr Tyr Phe
 35 40 45
 Leu Cys Gly Gln Pro Leu His Phe Ile Pro Arg Lys Gln Leu Cys Asp
 50 55 60
 Gly Glu Leu Asp Cys Pro Leu Gly Glu Asp Glu Glu His Cys Val Lys
 65 70 75 80
 Ser Phe Pro Glu Gly Pro Ala Val Ala Val Arg Leu Ser Lys Asp Arg
 85 90 95
 Ser Thr Leu Gln Val Leu Asp Ser Ala Thr Gly Asn Trp Phe Ser Ala
 100 105 110
 Cys Phe Asp Asn Phe Thr Glu Ala Leu Ala Glu Thr Ala Cys Arg Gln
 115 120 125
 Met Gly Tyr Ser Ser Lys Pro Thr Phe Arg Ala Val Glu Ile Gly Pro
 130 135 140
 Asp Gln Asp Leu Asp Val Val Glu Ile Thr Glu Asn Ser Gln Glu Leu
 145 150 155 160
 Arg Met Arg Asn Ser Ser Gly Pro Cys Leu Ser Gly Ser Leu Val Ser
 165 170 175
 Leu His Cys Leu Ala Cys Gly Lys Ser Leu Lys Thr Pro Arg Val Val
 180 185 190
 Gly Gly Glu Glu Ala Ser Val Asp Ser Trp Pro Trp Gln Val Ser Ile
 195 200 205
 Gln Tyr Asp Lys Gln His Val Cys Gly Gly Ser Ile Leu Asp Pro His
 210 215 220
 Trp Val Leu Thr Ala Ala His Cys Phe Arg Lys His Thr Asp Val Phe
 225 230 235 240
 Asn Trp Lys Val Arg Ala Gly Ser Asp Lys Leu Gly Ser Phe Pro Ser
 245 250 255
 Leu Ala Val Ala Lys Ile Ile Ile Ile Glu Phe Asn Pro Met Tyr Pro
 260 265 270
 Lys Asp Asn Asp Ile Ala Leu Met Lys Leu Gln Phe Pro Leu Thr Phe
 275 280 285
 Ser Gly Thr Val Arg Pro Ile Cys Leu Pro Phe Phe Asp Glu Glu Leu
 290 295 300
 Thr Pro Ala Thr Pro Leu Trp Ile Ile Gly Trp Gly Phe Thr Lys Gln
 305 310 315 320
 Asn Gly Gly Lys Met Ser Asp Ile Leu Leu Gln Ala Ser Val Gln Val

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      325      330      335
Ile Asp Ser Thr Arg Cys Asn Ala Asp Asp Ala Tyr Gln Gly Glu Val
      340      345      350
Thr Glu Lys Met Met Cys Ala Gly Ile Pro Glu Gly Gly Val Asp Thr
      355      360      365
Cys Gln Gly Asp Ser Gly Gly Pro Leu Met Tyr Gln Ser Asp Gln Trp
      370      375      380
His Val Val Gly Ile Val Ser Trp Gly Tyr Gly Cys Gly Gly Pro Ser
      385      390      395      400
Thr Pro Gly Val Tyr Thr Lys Val Ser Ala Tyr Leu Asn Trp Ile Tyr
      405      410      415
Asn Val Trp Lys Ala Glu Leu
      420

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<210> 40
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 <212> DNA
 <213> Artificial sequence

<220>
 <223> DESC1 gene

<221> misc feature
 <222> (626)...(1324)
 <223> protease domain

<221> CDS
 <222> (56)...(1324)

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<400> 40
tgacttggat gtagacctcg accttcacag gactcttcat tgctggttgg caatg atg      58
                                     Met
                                     1

tat cgg cca gat gtg gtg agg gct agg aaa aga gtt tgt tgg gaa ccc      106
Tyr Arg Pro Asp Val Val Arg Ala Arg Lys Arg Val Cys Trp Glu Pro
      5      10      15

tgg gtt atc ggc ctc gtc ats ttc ata tcc ctg att gtc ctg gca gtg      154
Trp Val Ile Gly Leu Val Xaa Phe Ile Ser Leu Ile Val Leu Ala Val
      20      25      30

tgc att gga stc act gtt cat tat gtg aga tat aat caa aag aag acc      202
Cys Ile Gly Xaa Thr Val His Tyr Val Arg Tyr Asn Gln Lys Lys Thr
      35      40      45

tac aat tac tat agc aca ttg tca ttt aca act gac aaa cta tat gct      250
Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr Thr Asp Lys Leu Tyr Ala
      50      55      60      65

gag ttt ggc aga gag gct tct aac aat ttt aca gaa atg agc cag aga      298
Glu Phe Gly Arg Glu Ala Ser Asn Asn Phe Thr Glu Met Ser Gln Arg
      70      75      80

ctt gaa tca atg gtg aaa aat gca ttt tat aaa tct cca tta agg gaa      346
Leu Glu Ser Met Val Lys Asn Ala Phe Tyr Lys Ser Pro Leu Arg Glu
      85      90      95

gaa ttt gtc aag tct cag gtt atc aag ttc agt caa cag aag cat gga      394
Glu Phe Val Lys Ser Gln Val Ile Lys Phe Ser Gln Gln Lys His Gly
      100      105      110

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gtg ttg gct cat atg ctg ttg att tgt aga ttt cac tct act gag gat Val Leu Ala His Met Leu Leu Ile Cys Arg Phe His Ser Thr Glu Asp 115 120 125	442
cct gaa act gta gat aaa att gtt caa ctt gtt tta cat gaa aag ctg Pro Glu Thr Val Asp Lys Ile Val Gln Leu Val Leu His Glu Lys Leu 130 135 140 145	490
caa gat gct gta gga ccc cct aaa gta gat cct cac tca gtt aaa att Gln Asp Ala Val Gly Pro Pro Lys Val Asp Pro His Ser Val Lys Ile 150 155 160	538
aaa aaa atc aac aag aca gaa aca gac agc tat cta aac cat tgc tgc Lys Lys Ile Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys Cys 165 170 175	586
gga aca cga aga agt aaa act cta ggt cag agt ctc agg atc gtt ggt Gly Thr Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val Gly 180 185 190	634
ggg aca gaa gta gaa gag ggt gaa tgg ccc tgg cag gct agc ctg cag Gly Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln 195 200 205	682
tgg gat ggg agt cat cgc tgt gga gca acc tta att aat gcc aca tgg Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile Asn Ala Thr Trp 210 215 220 225	730
ctt gtg agt gct gct cac tgt ttt aca aca tat aag aac cct gcc aga Leu Val Ser Ala Ala His Cys Phe Thr Thr Tyr Lys Asn Pro Ala Arg 230 235 240	778
tgg act gct tcc ttt gga gta aca ata aaa cct tcg aaa atg aaa cgg Trp Thr Ala Ser Phe Gly Val Thr Ile Lys Pro Ser Lys Met Lys Arg 245 250 255	826
ggt ctc cgg aga ata att gtc cat gaa aaa tac aaa cac cca tca cat Gly Leu Arg Arg Ile Ile Val His Glu Lys Tyr Lys His Pro Ser His 260 265 270	874
gac tat gat att tct ctt gca gag ctt tot agc cct gtt ccc tac aca Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser Pro Val Pro Tyr Thr 275 280 285	922
aat gca gta cat aga gtt tgt ctc cct gat gca tcc tat gag ttt caa Asn Ala Val His Arg Val Cys Leu Pro Asp Ala Ser Tyr Glu Phe Gln 290 295 300 305	970
cca ggt gat gtg atg ttt gtg aca gga ttt gga gca ctg aaa aat gat Pro Gly Asp Val Met Phe Val Thr Gly Phe Gly Ala Leu Lys Asn Asp 310 315 320	1018
ggt tac agt caa aat cat ctt cga caa gca cag gtg act ctc ata gac Gly Tyr Ser Gln Asn His Leu Arg Gln Ala Gln Val Thr Leu Ile Asp 325 330 335	1066
gct aca act tgc aat gaa cct caa gct tac aat gac gcc ata act cct Ala Thr Thr Cys Asn Glu Pro Gln Ala Tyr Asn Asp Ala Ile Thr Pro 340 345 350	1114

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aga atg tta tgt gct ggc tcc tta gaa gga aaa aca gat gca tgc cag 1162
 Arg Met Leu Cys Ala Gly Ser Leu Glu Gly Lys Thr Asp Ala Cys Gln
 355 360 365

ggc gac tct gga gga cca ctg gtt agt tca gat gct aga gat atc tgg 1210
 Gly Asp Ser Gly Gly Pro Leu Val Ser Ser Asp Ala Arg Asp Ile Trp
 370 375 380 385

tac ctt gct gga ata gtg agc tsg gga gat gaa tgt gcg aaa ccc aac 1258
 Tyr Leu Ala Gly Ile Val Ser Xaa Gly Asp Glu Cys Ala Lys Pro Asn
 390 395 400

aag cct ggt gtt tat act aga gtt acg gcc ttg cgg gac tgg att act 1306
 Lys Pro Gly Val Tyr Thr Arg Val Thr Ala Leu Arg Asp Trp Ile Thr
 405 410 415

tca aaa act ggt atc taa gagagaaaag cctcatggaa cagataacat 1354
 Ser Lys Thr Gly Ile *
 420

ttttttttgt tttttgggtg tggaggccat ttttagagat acagaattgg agaagacttg 1414
 caaaacagct agatttgact gatctcaata aactgtttgc ttgatgcaaa aaaaaaa 1471

<210> 41
 <211> 422
 <212> PRT
 <213> Homo Sapien

<220>
 <221> VARIANT
 <222> 24
 <223> Xaa is Ile or Met

<221> VARIANT
 <222> 37
 <223> Xaa is Leu or Val

<221> VARIANT
 <222> 393
 <223> Xaa is Ser or Trp

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 Pro Trp Val Ile Gly Leu Val Xaa Phe Ile Ser Leu Ile Val Leu Ala
 20 25 30
 Val Cys Ile Gly Xaa Thr Val His Tyr Val Arg Tyr Asn Gln Lys Lys
 35 40 45
 Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr Thr Asp Lys Leu Tyr
 50 55 60
 Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn Phe Thr Glu Met Ser Gln
 65 70 75 80
 Arg Leu Glu Ser Met Val Lys Asn Ala Phe Tyr Lys Ser Pro Leu Arg
 85 90 95
 Glu Glu Phe Val Lys Ser Gln Val Ile Lys Phe Ser Gln Gln Lys His
 100 105 110
 Gly Val Leu Ala His Met Leu Leu Ile Cys Arg Phe His Ser Thr Glu
 115 120 125
 Asp Pro Glu Thr Val Asp Lys Ile Val Gln Leu Val Leu His Glu Lys
 130 135 140
 Leu Gln Asp Ala Val Gly Pro Pro Lys Val Asp Pro His Ser Val Lys

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145      150      155      160
Ile Lys Lys Ile Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys
      165      170      175
Cys Gly Thr Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val
      180      185      190
Gly Gly Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu
      195      200      205
Gln Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile Asn Ala Thr
      210      215      220
Trp Leu Val Ser Ala Ala His Cys Phe Thr Thr Tyr Lys Asn Pro Ala
225      230      235      240
Arg Trp Thr Ala Ser Phe Gly Val Thr Ile Lys Pro Ser Lys Met Lys
      245      250      255
Arg Gly Leu Arg Arg Ile Ile Val His Glu Lys Tyr Lys His Pro Ser
      260      265      270
His Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser Pro Val Pro Tyr
      275      280      285
Thr Asn Ala Val His Arg Val Cys Leu Pro Asp Ala Ser Tyr Glu Phe
      290      295      300
Gln Pro Gly Asp Val Met Phe Val Thr Gly Phe Gly Ala Leu Lys Asn
305      310      315      320
Asp Gly Tyr Ser Gln Asn His Leu Arg Gln Ala Gln Val Thr Leu Ile
      325      330      335
Asp Ala Thr Thr Cys Asn Glu Pro Gln Ala Tyr Asn Asp Ala Ile Thr
      340      345      350
Pro Arg Met Leu Cys Ala Gly Ser Leu Glu Gly Lys Thr Asp Ala Cys
      355      360      365
Gln Gly Asp Ser Gly Gly Pro Leu Val Ser Ser Asp Ala Arg Asp Ile
      370      375      380
Trp Tyr Leu Ala Gly Ile Val Ser Xaa Gly Asp Glu Cys Ala Lys Pro
385      390      395      400
Asn Lys Pro Gly Val Tyr Thr Arg Val Thr Ala Leu Arg Asp Trp Ile
      405      410      415
Thr Ser Lys Thr Gly Ile
      420

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<210> 42

<211> 1257

<212> DNA

<213> Homo sapien

<220>

<221> CDS

<222> (1)...(1257)

<223> Nucleotide sequence encoding MTSP9

<400> 42

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atg atg tat cgg aca gta gga ttt ggc acc cga agc aga aat ctg aag      48
Met Met Tyr Arg Thr Val Gly Phe Gly Thr Arg Ser Arg Asn Leu Lys
  1           5           10           15

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cca tgg atg att gcc gtt ctc att gtg ttg tcc ctg aca gtg gtg gca      96
Pro Trp Met Ile Ala Val Leu Ile Val Leu Ser Leu Thr Val Val Ala
      20           25           30

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gtg acc ata ggt ctc ctg gtt cac ttc cta gta ttt gac caa aaa aag      144
Val Thr Ile Gly Leu Leu Val His Phe Leu Val Phe Asp Gln Lys Lys
      35           40           45

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gag tac tat cat ggc tcc ttt aaa att tta gat cca caa atc aat aac      192
Glu Tyr Tyr His Gly Ser Phe Lys Ile Leu Asp Pro Gln Ile Asn Asn

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50	55	60	
aat ttc gga caa agc aac	aca tat caa ctt aag	gac tta cga gag acg	240
Asn Phe Gly Gln Ser Asn	Thr Tyr Gln Leu Lys	Asp Leu Arg Glu Thr	
65	70	75 80	
acc gaa aat ttg gtg gat	gag ata ttt ata gat	tca gcc tgg aag aaa	288
Thr Glu Asn Leu Val Asp	Glu Ile Phe Ile Asp	Ser Ala Trp Lys Lys	
	85	90 95	
aat tat atc aag aac caa	gta gtc aga ctg act cca	gag gaa gat ggt	336
Asn Tyr Ile Lys Asn Gln	Val Val Arg Leu Thr	Pro Glu Glu Asp Gly	
	100	105 110	
gtg aaa gta gat gtc att	atg gtg ttc cag ttc	ccc tct act gaa caa	384
Val Lys Val Asp Val Ile	Met Val Phe Gln Phe	Pro Ser Thr Glu Gln	
	115	120 125	
agg gca gta aga gag aag	aaa atc caa agc atc	tta aat cag aag ata	432
Arg Ala Val Arg Glu Lys	Lys Ile Gln Ser Ile	Leu Asn Gln Lys Ile	
	130	135 140	
agg aat tta aga gcc ttg	cca ata aat gcc tca	tca gtt caa gtt aat	480
Arg Asn Leu Arg Ala Leu	Pro Ile Asn Ala Ser	Ser Val Gln Val Asn	
	145	150 155 160	
gca atg agc tca tca aca	ggg gag tta act gtc	caa gca agt tgt ggt	528
Ala Met Ser Ser Thr Gly	Glu Leu Thr Val Gln	Ala Ser Cys Gly	
	165	170 175	
aaa cga gtt gtt cca tta	aac gtc aac aga ata	gca tct gga gtc att	576
Lys Arg Val Val Pro Leu	Asn Val Asn Arg Ile	Ala Ser Gly Val Ile	
	180	185 190	
gca ccc aag gcg gcc tgg	cct tgg caa gct tcc	ctt cag tat gat aac	624
Ala Pro Lys Ala Ala Trp	Pro Trp Gln Ala Ser	Leu Gln Tyr Asp Asn	
	195	200 205	
atc cat cag tgt ggg gcc	acc ttg att agt aac	aca tgg ctt gtc act	672
Ile His Gln Cys Gly Ala	Thr Leu Ile Ser Asn	Thr Trp Leu Val Thr	
	210	215 220	
gca gca cac tgc ttc cag	aag tat aaa aat cca	cat caa tgg act gtt	720
Ala Ala His Cys Phe Gln	Lys Tyr Lys Asn Pro	His Gln Trp Thr Val	
	225	230 235 240	
agt ttt gga aca aaa atc	aac cct ccc tta atg	aaa aga aat gtc aga	768
Ser Phe Gly Thr Lys Ile	Asn Pro Pro Leu Met	Lys Arg Asn Val Arg	
	245	250 255	
aga ttt att atc cat gag	aag tac cgc tct gca	gca aga gag tac gac	816
Arg Phe Ile Ile His Glu	Lys Tyr Arg Ser Ala	Ala Ala Arg Glu Tyr Asp	
	260	265 270	
att gct gtt gtg cag gtc	tct tcc aga gtc acc	ttt tcg gat gac ata	864
Ile Ala Val Val Gln Val	Ser Ser Arg Val Thr	Phe Ser Asp Asp Ile	
	275	280 285	
cgc cgg att tgt ttg cca	gaa gcc tct gca tcc	ttc caa cca aat ttg	912
Arg Arg Ile Cys Leu Pro	Glu Ala Ser Ala Ser	Phe Gln Pro Asn Leu	
	290	295 300	

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act gtc cac atc aca gga ttt gga gca ctt tac tat ggt ggg gaa tcc 960
 Thr Val His Ile Thr Gly Phe Gly Ala Leu Tyr Tyr Gly Gly Glu Ser
 305 310 315 320

caa aat gat ctc cga gaa gcc aga gtg aaa atc ata agt gac gat gtc 1008
 Gln Asn Asp Leu Arg Glu Ala Arg Val Lys Ile Ile Ser Asp Asp Val
 325 330 335

tgc aag caa cca cag gtg tat ggc aat gat ata aaa cct gga atg ttc 1056
 Cys Lys Gln Pro Gln Val Tyr Gly Asn Asp Ile Lys Pro Gly Met Phe
 340 345 350

tgt gcc gga tat atg gaa gga att tat gat gcc tgc agg ggt gat tct 1104
 Cys Ala Gly Tyr Met Glu Gly Ile Tyr Asp Ala Cys Arg Gly Asp Ser
 355 360 365

ggg gga cct tta gtc aca agg gat ctg aaa gat acg tgg tat ctc att 1152
 Gly Gly Pro Leu Val Thr Arg Asp Leu Lys Asp Thr Trp Tyr Leu Ile
 370 375 380

gga att gta agc tgg gga gat aac tgt ggt caa aag gac aag cct gga 1200
 Gly Ile Val Ser Trp Gly Asp Asn Cys Gly Gln Lys Asp Lys Pro Gly
 385 390 395 400

gtc tac aca caa gtg act tat tac cga aac tgg att gct tca aaa aca 1248
 Val Tyr Thr Gln Val Thr Tyr Tyr Arg Asn Trp Ile Ala Ser Lys Thr
 405 410 415

ggc atc taa 1257
 Gly Ile *

<210> 43
 <211> 418
 <212> PRT
 <213> Homo sapien

<400> 43
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 Val Thr Ile Gly Leu Leu Val His Phe Leu Val Phe Asp Gln Lys Lys
 35 40 45
 Glu Tyr Tyr His Gly Ser Phe Lys Ile Leu Asp Pro Gln Ile Asn Asn
 50 55 60
 Asn Phe Gly Gln Ser Asn Thr Tyr Gln Leu Lys Asp Leu Arg Glu Thr
 65 70 75 80
 Thr Glu Asn Leu Val Asp Glu Ile Phe Ile Asp Ser Ala Trp Lys Lys
 85 90 95
 Asn Tyr Ile Lys Asn Gln Val Val Arg Leu Thr Pro Glu Glu Asp Gly
 100 105 110
 Val Lys Val Asp Val Ile Met Val Phe Gln Phe Pro Ser Thr Glu Gln
 115 120 125
 Arg Ala Val Arg Glu Lys Lys Ile Gln Ser Ile Leu Asn Gln Lys Ile
 130 135 140
 Arg Asn Leu Arg Ala Leu Pro Ile Asn Ala Ser Ser Val Gln Val Asn
 145 150 155 160
 Ala Met Ser Ser Ser Thr Gly Glu Leu Thr Val Gln Ala Ser Cys Gly
 165 170 175

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Lys Arg Val Val Pro Leu Asn Val Asn Arg Ile Ala Ser Gly Val Ile
 180 185 190
 Ala Pro Lys Ala Ala Trp Pro Trp Gln Ala Ser Leu Gln Tyr Asp Asn
 195 200 205
 Ile His Gln Cys Gly Ala Thr Leu Ile Ser Asn Thr Trp Leu Val Thr
 210 215 220
 Ala Ala His Cys Phe Gln Lys Tyr Lys Asn Pro His Gln Trp Thr Val
 225 230 235 240
 Ser Phe Gly Thr Lys Ile Asn Pro Pro Leu Met Lys Arg Asn Val Arg
 245 250 255
 Arg Phe Ile Ile His Glu Lys Tyr Arg Ser Ala Ala Arg Glu Tyr Asp
 260 265 270
 Ile Ala Val Val Gln Val Ser Ser Arg Val Thr Phe Ser Asp Asp Ile
 275 280 285
 Arg Arg Ile Cys Leu Pro Glu Ala Ser Ala Ser Phe Gln Pro Asn Leu
 290 295 300
 Thr Val His Ile Thr Gly Phe Gly Ala Leu Tyr Tyr Gly Gly Glu Ser
 305 310 315 320
 Gln Asn Asp Leu Arg Glu Ala Arg Val Lys Ile Ile Ser Asp Asp Val
 325 330 335
 Cys Lys Gln Pro Gln Val Tyr Gly Asn Asp Ile Lys Pro Gly Met Phe
 340 345 350
 Cys Ala Gly Tyr Met Glu Gly Ile Tyr Asp Ala Cys Arg Gly Asp Ser
 355 360 365
 Gly Gly Pro Leu Val Thr Arg Asp Leu Lys Asp Thr Trp Tyr Leu Ile
 370 375 380
 Gly Ile Val Ser Trp Gly Asp Asn Cys Gly Gln Lys Asp Lys Pro Gly
 385 390 395 400
 Val Tyr Thr Gln Val Thr Tyr Tyr Arg Asn Trp Ile Ala Ser Lys Thr
 405 410 415
 Gly Ile

<210> 44

<211> 2130

<212> DNA

<213> Homo Sapien

<220>

<221> CDS

<222> (0)...(2104)

 <223> Nucleotide sequence encoding MTSP10, including
 MTSP10 protease domain

<400> 44

ata aac ctg gtt tat aca aca tct gcc ttc tcc aaa ttt tat gag cag 48
 ile Asn Leu Val Tyr Thr Thr Ser Ala Phe Ser Lys Phe Tyr Glu Gln
 1 5 10 15

tct gtt gtt gca gat gtc agc agc aac aac aaa ggc ggc ctc ctt gtc 96
 Ser Val Val Ala Asp Val Ser Ser Asn Asn Lys Gly Gly Leu Leu Val
 20 25 30

cac ttt tgg att gtt ttt gtc atg cca cgt gcc aaa ggc cac atc ttc 144
 His Phe Trp Ile Val Phe Val Met Pro Arg Ala Lys Gly His Ile Phe
 35 40 45

tgt gaa gac tgt gtt gcc gcc atc ttg aag gac tcc atc cag aca agc 192
 Cys Glu Asp Cys Val Ala Ala Ile Leu Lys Asp Ser Ile Gln Thr Ser
 50 55 60

atc ata aac cgg acc tct gtg ggg agc ttg cag gga ctg gct gtg gac 240

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Ile 65	Ile	Asn	Arg	Thr	Ser 70	Val	Gly	Ser	Leu	Gln 75	Gly	Leu	Ala	Val	Asp 80	
atg	gac	tct	gtg	gta	cta	aat	gct	ggg	ctt	cgg	tca	gat	tac	tcg	tca	288
Met	Asp	Ser	Val	Val	Leu	Asn	Ala	Gly	Leu	Arg	Ser	Asp	Tyr	Ser	Ser	
					85				90					95		
acc	ata	gga	tct	gac	aaa	ggc	tgc	tct	cag	tac	ttc	tat	gca	gag	cat	336
Thr	Ile	Gly	Ser	Asp	Lys	Gly	Cys	Ser	Gln	Tyr	Phe	Tyr	Ala	Glu	His	
			100					105					110			
ctg	tct	ctc	cac	tac	ccg	ctg	gag	att	tct	gca	gcc	tca	ggg	agg	ctg	384
Leu	Ser	Leu	His	Tyr	Pro	Leu	Glu	Ile	Ser	Ala	Ala	Ser	Gly	Arg	Leu	
			115				120					125				
atg	tgt	cac	ttc	aag	ctg	gtg	gcc	ata	gtg	ggc	tac	ctg	att	cgt	ctc	432
Met	Cys	His	Phe	Lys	Leu	Val	Ala	Ile	Val	Gly	Tyr	Leu	Ile	Arg	Leu	
	130					135					140					
tca	atc	aag	tcc	atc	caa	atc	gaa	gcc	gac	aac	tgt	gtc	act	gac	tcc	480
Ser	Ile	Lys	Ser	Ile	Gln	Ile	Glu	Ala	Asp	Asn	Cys	Val	Thr	Asp	Ser	
145					150					155					160	
ctg	acc	att	tac	gac	tcc	ctt	ttg	ccc	atc	cgg	agc	agc	atc	ttg	tac	528
Leu	Thr	Ile	Tyr	Asp	Ser	Leu	Leu	Pro	Ile	Arg	Ser	Ser	Ile	Leu	Tyr	
				165					170					175		
aga	att	tgt	gaa	ccc	aca	aga	aca	tta	atg	tca	ttt	gtt	tct	aca	aat	576
Arg	Ile	Cys	Glu	Pro	Thr	Arg	Thr	Leu	Met	Ser	Phe	Val	Ser	Thr	Asn	
			180					185					190			
aat	ctc	atg	ttg	gtg	aca	ttt	aag	tct	cct	cat	ata	cgg	agg	ctc	tca	624
Asn	Leu	Met	Leu	Val	Thr	Phe	Lys	Ser	Pro	His	Ile	Arg	Arg	Leu	Ser	
		195					200					205				
gga	atc	cgg	gca	tat	ttt	gag	gtc	att	cca	gaa	caa	aag	tgt	gaa	aac	672
Gly	Ile	Arg	Ala	Tyr	Phe	Glu	Val	Ile	Pro	Glu	Gln	Lys	Cys	Glu	Asn	
	210					215					220					
aca	gtg	ttg	gtc	aaa	gac	atc	act	ggc	ttt	gaa	ggg	aaa	att	tca	agc	720
Thr	Val	Leu	Val	Lys	Asp	Ile	Thr	Gly	Phe	Glu	Gly	Lys	Ile	Ser	Ser	
225				230				235						240		
cca	tat	tac	ccg	agc	tac	tat	cct	cca	aaa	tgc	aag	tgt	acc	tgg	aaa	768
Pro	Tyr	Tyr	Pro	Ser	Tyr	Tyr	Pro	Pro	Lys	Cys	Lys	Cys	Thr	Trp	Lys	
				245				250						255		
ttt	cag	act	tct	cta	tca	act	ctt	ggc	ata	gca	ctg	aaa	ttc	tat	aac	816
Phe	Gln	Thr	Ser	Leu	Ser	Thr	Leu	Gly	Ile	Ala	Leu	Lys	Phe	Tyr	Asn	
			260					265					270			
tat	tca	ata	acc	aag	aag	agt	atg	aaa	ggc	tgt	gag	cat	gga	tgg	tgg	864
Tyr	Ser	Ile	Thr	Lys	Lys	Ser	Met	Lys	Gly	Cys	Glu	His	Gly	Trp	Trp	
		275					280					285				
gaa	att	tat	gag	cac	atg	tac	tgt	ggc	tcc	tac	atg	gat	cat	cag	aca	912
Glu	Ile	Tyr	Glu	His	Met	Tyr	Cys	Gly	Ser	Tyr	Met	Asp	His	Gln	Thr	
	290					295					300					
att	ttt	cga	gtg	ccc	agc	cct	ctg	gtt	cac	att	cag	ctc	cag	tgc	agt	960
Ile	Phe	Arg	Val	Pro	Ser	Pro	Leu	Val	His	Ile	Gln	Leu	Gln	Cys	Ser	

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305	310	315	320	
tca agg ctt tca ggc aag cca ctt ttg gca gaa tat ggc agt tac aac Ser Arg Leu Ser Gly Lys Pro Leu Leu Ala Glu Tyr Gly Ser Tyr Asn 325 330 335				1008
atc agt caa ccc tgc cct gtg gga tct ttt aga tgc tcc tcc ggt tta Ile Ser Gln Pro Cys Pro Val Gly Ser Phe Arg Cys Ser Ser Gly Leu 340 345 350				1056
tgt gtc cct cag gcc cag cgt ggt gat gga gta aat gac tgc ttt gat Cys Val Pro Gln Ala Gln Arg Gly Asp Gly Val Asn Asp Cys Phe Asp 355 360 365				1104
gaa agt gat gaa ctg ttt tgc gtg agc cct caa cct gcc tgc aat acc Glu Ser Asp Glu Leu Phe Cys Val Ser Pro Gln Pro Ala Cys Asn Thr 370 375 380				1152
agc tcc ttc agg cag cat ggc cct ctc atc tgt gat ggc ttc agg gac Ser Ser Phe Arg Gln His Gly Pro Leu Ile Cys Asp Gly Phe Arg Asp 385 390 400				1200
tgt gag aat ggc cgg gat gag caa aac tgc act caa agt att cca tgc Cys Glu Asn Gly Arg Asp Glu Gln Asn Cys Thr Gln Ser Ile Pro Cys 405 410 415				1248
aac aac aga act ttt aag tgt ggc aat gat att tgc ttt agg aaa caa Asn Asn Arg Thr Phe Lys Cys Gly Asn Asp Ile Cys Phe Arg Lys Gln 420 425 430				1296
aat gca aaa tgt gat ggg aca gtg gat tgt cca gat gga agt gat gaa Asn Ala Lys Cys Asp Gly Thr Val Asp Cys Pro Asp Gly Ser Asp Glu 435 440 445				1344
gaa ggc tgc acc tgc agc agg agt tcc tcc gcc ctt cac cgc atc atc Glu Gly Cys Thr Cys Ser Arg Ser Ser Ser Ala Leu His Arg Ile Ile 450 455 460				1392
gga ggc aca gac acc ctg gag ggg ggt tgg ccg tgg cag gtc agc ctc Gly Gly Thr Asp Thr Leu Glu Gly Gly Trp Pro Trp Gln Val Ser Leu 465 470 475 480				1440
cac ttt gtt gga tct gcc tac tgt ggt gcc tca gtc atc tcc agg gag His Phe Val Gly Ser Ala Tyr Cys Gly Ala Ser Val Ile Ser Arg Glu 485 490 495				1488
tgg ctt ctt tct gca gcc cac tgt ttt cat gga aac agg ctg tca gat Trp Leu Leu Ser Ala Ala His Cys Phe His Gly Asn Arg Leu Ser Asp 500 505 510				1536
ccc aca cca tgg act gca cac ctc ggg atg tat gtt cag ggg aat gcc Pro Thr Pro Trp Thr Ala His Leu Gly Met Tyr Val Gln Gly Asn Ala 515 520 525				1584
aag ttt gtc tcc ccg gtg aga aga att gtg gtc cac gag tac tat aac Lys Phe Val Ser Pro Val Arg Arg Ile Val Val His Glu Tyr Tyr Asn 530 535 540				1632
agt cag act ttt gat tat gat att gct ttg cta cag ctc agt att gcc Ser Gln Thr Phe Asp Tyr Asp Ile Ala Leu Gln Leu Ser Ile Ala 545 550 555 560				1680

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tgg cct gag acc ctg aaa cag ctc att cag cca ata tgc att cct ccc	1728
Trp Pro Glu Thr Leu Lys Gln Leu Ile Gln Pro Ile Cys Ile Pro Pro	
565 570 575	
act ggt cag aga gtt cgc agt ggg gag aag tgc tgg gta act ggc tgg	1776
Thr Gly Gln Arg Val Arg Ser Gly Glu Lys Cys Trp Val Thr Gly Trp	
580 585 590	
ggg cga aga cac gaa gca gat aat aaa ggc tcc ctc gtt ctg cag caa	1824
Gly Arg Arg His Glu Ala Asp Asn Lys Gly Ser Leu Val Leu Gln Gln	
595 600 605	
gcg gag gta gag ctc att gat caa acg ctc tgt gtt tcc acc tac ggg	1872
Ala Glu Val Glu Leu Ile Asp Gln Thr Leu Cys Val Ser Thr Tyr Gly	
610 615 620	
atc atc act tct cgg atg ctc tgt gca ggc ata atg tca ggc aag aga	1920
Ile Ile Thr Ser Arg Met Leu Cys Ala Gly Ile Met Ser Gly Lys Arg	
625 630 635 640	
gat gcc tgc aaa gga gat tgc ggt gga cct tta tct tgt cga aga aaa	1968
Asp Ala Cys Lys Gly Asp Ser Gly Gly Pro Leu Ser Cys Arg Arg Lys	
645 650 655	
agt gat gga aaa tgg att ttg act ggc att gtt agc tgg gga cat gga	2016
Ser Asp Gly Lys Trp Ile Leu Thr Gly Ile Val Ser Trp Gly His Gly	
660 665 670	
tgt gga cga cca aac ttt cct ggt gtt tac aca agg gtg tca aac ttt	2064
Cys Gly Arg Pro Asn Phe Pro Gly Val Tyr Thr Arg Val Ser Asn Phe	
675 680 685	
gtt ccc tgg att cat aaa tat gtc cct tct ctt ttg taa t tgcaaaaaaa	2114
Val Pro Trp Ile His Lys Tyr Val Pro Ser Leu Leu *	
690 695 700	
aaaaaaaaa aaaaaa	2130
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<211> 700	
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<213> Homo Sapien	
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His Phe Trp Ile Val Phe Val Met Pro Arg Ala Lys Gly His Ile Phe	
35 40 45	
Cys Glu Asp Cys Val Ala Ala Ile Leu Lys Asp Ser Ile Gln Thr Ser	
50 55 60	
Ile Ile Asn Arg Thr Ser Val Gly Ser Leu Gln Gly Leu Ala Val Asp	
65 70 75 80	
Met Asp Ser Val Val Leu Asn Ala Gly Leu Arg Ser Asp Tyr Ser Ser	
85 90 95	
Thr Ile Gly Ser Asp Lys Gly Cys Ser Gln Tyr Phe Tyr Ala Glu His	
100 105 110	
Leu Ser Leu His Tyr Pro Leu Glu Ile Ser Ala Ala Ser Gly Arg Leu	
115 120 125	

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Met Cys His Phe Lys Leu Val Ala Ile Val Gly Tyr Leu Ile Arg Leu
 130 135 140
 Ser Ile Lys Ser Ile Gln Ile Glu Ala Asp Asn Cys Val Thr Asp Ser
 145 150 155 160
 Leu Thr Ile Tyr Asp Ser Leu Leu Pro Ile Arg Ser Ser Ile Leu Tyr
 165 170 175
 Arg Ile Cys Glu Pro Thr Arg Thr Leu Met Ser Phe Val Ser Thr Asn
 180 185 190
 Asn Leu Met Leu Val Thr Phe Lys Ser Pro His Ile Arg Arg Leu Ser
 195 200 205
 Gly Ile Arg Ala Tyr Phe Glu Val Ile Pro Glu Gln Lys Cys Glu Asn
 210 215 220
 Thr Val Leu Val Lys Asp Ile Thr Gly Phe Glu Gly Lys Ile Ser Ser
 225 230 235 240
 Pro Tyr Tyr Pro Ser Tyr Tyr Pro Pro Lys Cys Lys Cys Thr Trp Lys
 245 250 255
 Phe Gln Thr Ser Leu Ser Thr Leu Gly Ile Ala Leu Lys Phe Tyr Asn
 260 265 270
 Tyr Ser Ile Thr Lys Lys Ser Met Lys Gly Cys Glu His Gly Trp Trp
 275 280 285
 Glu Ile Tyr Glu His Met Tyr Cys Gly Ser Tyr Met Asp His Gln Thr
 290 295 300
 Ile Phe Arg Val Pro Ser Pro Leu Val His Ile Gln Leu Gln Cys Ser
 305 310 315 320
 Ser Arg Leu Ser Gly Lys Pro Leu Leu Ala Glu Tyr Gly Ser Tyr Asn
 325 330 335
 Ile Ser Gln Pro Cys Pro Val Gly Ser Phe Arg Cys Ser Ser Gly Leu
 340 345 350
 Cys Val Pro Gln Ala Gln Arg Gly Asp Gly Val Asn Asp Cys Phe Asp
 355 360 365
 Glu Ser Asp Glu Leu Phe Cys Val Ser Pro Gln Pro Ala Cys Asn Thr
 370 375 380
 Ser Ser Phe Arg Gln His Gly Pro Leu Ile Cys Asp Gly Phe Arg Asp
 385 390 395 400
 Cys Glu Asn Gly Arg Asp Glu Gln Asn Cys Thr Gln Ser Ile Pro Cys
 405 410 415
 Asn Asn Arg Thr Phe Lys Cys Gly Asn Asp Ile Cys Phe Arg Lys Gln
 420 425 430
 Asn Ala Lys Cys Asp Gly Thr Val Asp Cys Pro Asp Gly Ser Asp Glu
 435 440 445
 Glu Gly Cys Thr Cys Ser Arg Ser Ser Ser Ala Leu His Arg Ile Ile
 450 455 460
 Gly Gly Thr Asp Thr Leu Glu Gly Gly Trp Pro Trp Gln Val Ser Leu
 465 470 475 480
 His Phe Val Gly Ser Ala Tyr Cys Gly Ala Ser Val Ile Ser Arg Glu
 485 490 495
 Trp Leu Leu Ser Ala Ala His Cys Phe His Gly Asn Arg Leu Ser Asp
 500 505 510
 Pro Thr Pro Trp Thr Ala His Leu Gly Met Tyr Val Gln Gly Asn Ala
 515 520 525
 Lys Phe Val Ser Pro Val Arg Arg Ile Val Val His Glu Tyr Tyr Asn
 530 535 540
 Ser Gln Thr Phe Asp Tyr Asp Ile Ala Leu Leu Gln Leu Ser Ile Ala
 545 550 555 560
 Trp Pro Glu Thr Leu Lys Gln Leu Ile Gln Pro Ile Cys Ile Pro Pro
 565 570 575
 Thr Gly Gln Arg Val Arg Ser Gly Glu Lys Cys Trp Val Thr Gly Trp
 580 585 590
 Gly Arg Arg His Glu Ala Asp Asn Lys Gly Ser Leu Val Leu Gln Gln
 595 600 605
 Ala Glu Val Glu Leu Ile Asp Gln Thr Leu Cys Val Ser Thr Tyr Gly

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610		615		620											
Ile	Ile	Thr	Ser	Arg	Met	Leu	Cys	Ala	Gly	Ile	Met	Ser	Gly	Lys	Arg
625					630					635					640
Asp	Ala	Cys	Lys	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Ser	Cys	Arg	Arg	Lys
				645					650					655	
Ser	Asp	Gly	Lys	Trp	Ile	Leu	Thr	Gly	Ile	Val	Ser	Trp	Gly	His	Gly
			660					665					670		
Cys	Gly	Arg	Pro	Asn	Phe	Pro	Gly	Val	Tyr	Thr	Arg	Val	Ser	Asn	Phe
		675					680					685			
Val	Pro	Trp	Ile	His	Lys	Tyr	Val	Pro	Ser	Leu	Leu				
	690					695					700				

<210> 46

<211> 8

<212> PRT

<213> Artificial sequence

<220>

<223> Conjugate

<221> MOD_RES

<222> 1

<221> MOD_RES

<222> 4

<223> Xaa is Quat: (R)-Glu(alpha-(3-amidinobenzyl))

<221> MOD_RES

<222> 8

<223> Alanine-therapeutic agent

<400> 46

Leu Arg Ala Xaa Gly Arg Ala Xaa

1

5

<210> 47

<211> 8

<212> PRT

<213> Artificial sequence

<220>

<223> Conjugate

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<222> 1

<221> MOD_RES

<222> 4

<223> Quat: (R)-Glu(alpha-(3-amidinobenzyl))

<221> MOD_RES

<222> 8

<223> Xaa is Alanine-therapeutic agent

<400> 47

Leu Arg Ala Xaa Ala Arg Ala Xaa

1

5

<210> 48

<211> 8

<212> PRT

-92-

<213> Artificial sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 4

<223> Xaa is Quat: (R)-Glu(alpha-(3-amidinobenzyl))

<221> MOD_RES

<222> 8

<223> Alanine-therapeutic agent

<400> 48

Leu Arg Ser Xaa Gly Arg Ala Xaa
1 5

<210> 49

<211> 8

<212> PRT

<213> Artificial sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 4

<223> Xaa is Quat: (R)-Glu(alpha-(3-amidinobenzyl))

<221> MOD_RES

<222> 8

<223> Alanine-therapeutic agent

<400> 49

Leu Arg Ser Xaa Ala Arg Ala Xaa
1 5

<210> 50

<211> 8

<212> PRT

<213> Artificial sequence

<220>

<223> Conjugate

<221> MOD_RES

<222> 1

<221> MOD_RES

<222> 8

<223> Isoleucine-therapeutic agent

<400> 50

Leu Arg Pro Arg Phe Lys Ile Xaa
1 5

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<210> 51
<211> 7
<212> PRT
<213> Artificial sequence

<220>
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<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Isoleucine-therapeutic agent

<400> 51
Arg Pro Arg Phe Lys Ile Xaa
1 5

<210> 52
<211> 6
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<220>
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<221> ACETYLATION
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<221> MOD_RES
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<223> Isoleucine-therapeutic agent

<400> 52
Pro Arg Phe Lys Ile Xaa
1 5

<210> 53
<211> 8
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<213> Artificial sequence

<220>
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<221> ACETYLATION
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<221> MOD_RES
<222> 8
<223> Alanine-therapeutic agent

<400> 53
Leu Arg Ser Lys Ser Arg Ala Xaa
1 5

<210> 54
<211> 7
<212> PRT
<213> Artificial sequence

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<220>
<223> Conjugate

<221> ACETYLATION
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<221> MOD_RES
<222> 7
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<400> 54
Arg Ser Lys Ser Arg Ala Xaa
1 5

<210> 55
<211> 6
<212> PRT
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<220>
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<221> ACETYLATION
<222> 1

<221> MOD_RES
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<223> Alanine-therapeutic agent

<400> 55
Ser Lys Ser Arg Ala Xaa
1 5

<210> 56
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<220>
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<221> ACETYLATION
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<222> 8
<223> Isoleucine-therapeutic agent

<400> 56
Leu Arg Pro Arg Phe Arg Ile Xaa
1 5

<210> 57
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<212> PRT
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<220>
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<221> ACETYLATION

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<222> 1
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<222> 7
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<400> 57
Arg Pro Arg Phe Arg Ile Xaa
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<210> 58
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<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Isoleucine-therapeutic agent

<400> 58
Pro Arg Phe Arg Ile Xaa
1 5

<210> 59
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<221> ACETYLATION
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<221> MOD_RES
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<400> 59
Leu Arg Ser Arg Ser Arg Ala Xaa
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<210> 60
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<212> PRT
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<220>
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<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7

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<223> Alanine-therapeutic agent

<400> 60

Arg Ser Arg Ser Arg Ala Xaa
1 5

<210> 61

<211> 6

<212> PRT

<213> Artificial sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 6

<223> Alanine-therapeutic agent

<400> 61

Ser Arg Ser Arg Ala Xaa
1 5

<210> 62

<211> 8

<212> PRT

<213> Artificial sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 4

<223> Xaa is Quat: (R)-Glu(alpha-(3-amidinobenzyl))

<221> MOD_RES

<222> 8

<223> Alanine-therapeutic agent

<400> 62

Leu Arg Ala Xaa Gly Arg Ala Xaa
1 5

<210> 63

<211> 8

<212> PRT

<213> Artificial sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 4

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<223> Xaa is Quat: (R)-Glu(alpha-(3-amidinobenzyl))

<221> MOD_RES

<222> 8

<223> Alanine-therapeutic agent

<400> 63

Leu Arg Ala Xaa Ala Arg Ala Xaa
1 5

<210> 64

<211> 8

<212> PRT

<213> Artificial sequence

<220>

<223> Conjugate

<221> ACETYLTATION

<222> 1

<221> MOD_RES

<222> 4

<223> Xaa is Quat: (R)-Glu(alpha-(3-amidinobenzyl))

<221> MOD_RES

<222> 8

<223> Alanine-therapeutic agent

<400> 64

Leu Arg Ser Xaa Gly Arg Ala Xaa
1 5

<210> 65

<211> 8

<212> PRT

<213> Artificial sequence

<220>

<223> Conjugate

<221> ACETYLTATION

<222> 1

<221> MOD_RES

<222> 4

<223> Xaa is Quat:
(R)-Glu(alpha-(3-amidinobenzyl))

<221> MOD_RES

<222> 8

<223> Alanine-therapeutic agent

<400> 65

Leu Arg Ser Xaa Ala Arg Ala Xaa
1 5

<210> 66

<211> 8

<212> PRT

<213> Artificial sequence

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<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
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<223> Isoleucine-therapeutic agent

<400> 66
Leu Arg Pro Arg Phe Lys Ile Xaa
1 5

<210> 67
<211> 7
<212> PRT
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<221> ACETYLATION
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<221> MOD_RES
<222> 7
<223> Isoleucine-therapeutic agent

<400> 67
Arg Pro Arg Phe Lys Ile Xaa
1 5

<210> 68
<211> 6
<212> PRT
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<220>
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<221> ACETYLATION
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<221> MOD_RES
<222> 6
<223> Isoleucine-therapeutic agent

<400> 68
Pro Arg Phe Lys Ile Xaa
1 5

<210> 69
<211> 8
<212> PRT
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<220>
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<221> ACETYLATION

-99-

<222> 1
<221> MOD_RES
<222> 8
<223> Alanine-therapeutic agent

<400> 69
Leu Arg Ser Lys Ser Arg Ala Xaa
1 5

<210> 70
<211> 7
<212> PRT
<213> Artificial Sequence

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<221> ACETYLATION
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<221> MOD_RES
<222> 7
<223> Alanine-therapeutic agent

<400> 70
Arg Ser Lys Ser Arg Ala Xaa
1 5

<210> 71
<211> 6
<212> PRT
<213> Artifical sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> (1)...(0)

<221> MOD_RES
<222> 6
<223> Alanine-therapeutic agent

<400> 71
Ser Lys Ser Arg Ala Xaa
1 5

<210> 72
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8

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<223> Isoleucine-therapeutic agent

<400> 72

Leu Arg Pro Arg Phe Arg Ile Xaa
1 5

<210> 73

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 7

<223> Isoleucine-therapeutic agent

<400> 73

Arg Pro Arg Phe Arg Ile Xaa
1 5

<210> 74

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 6

<223> Isoleucine-therapeutic agent

<400> 74

Pro Arg Phe Arg Ile Xaa
1 5

<210> 75

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 8

<223> Alanine-Therapeutic Agent

<400> 75

Leu Arg Ser Arg Ser Arg Ala Xaa

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1 5

<210> 76
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
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<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Alanine-therapeutic agent

<400> 76
Arg Ser Arg Ser Arg Ala Xaa
1 5

<210> 77
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Alanine-therapeutic agent

<400> 77
Ser Arg Ser Arg Ala Xaa
1 5

<210> 78
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is pyroglutamic acid

<221> MOD_RES
<222> 5
<223> Alanine-therapeutic agent

<400> 78
Xaa Pro Arg Ala Xaa
1 5

<210> 79

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<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is CH3SO2-D-HHT:
HHT is hexahydrotyrosol

<221> MOD_RES
<222> 5
<223> Alanine-therapeutic agent

<400> 79
Xaa Gly Arg Ala Xaa
1 5

<210> 80
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is N-p-tosyl-Gly

<221> MOD_RES
<222> 5
<223> Alanine-therapeutic agent

<400> 80
Xaa Pro Arg Ala Xaa
1 5

<210> 81
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is Benzoyl-Val

<221> MOD_RES
<222> 5
<223> Alanine-therapeutic agent

<400> 81
Xaa Gly Arg Ala Xaa
1 5

<210> 82

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<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is CH3SO2-D-HHT:
HHT is hexahydrotyrosyl

<221> MOD_RES
<222> 5
<223> Alanine-therapeutic agent

<400> 82
Xaa Gly Arg Ala Xaa
1 5

<210> 83
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is N-alpha-Z-D-Arg:
Z is benzyloxycarbonyl

<221> MOD_RES
<222> 5
<223> Alanine-therapeutic agent

<400> 83
Xaa Gly Arg Ala Xaa
1 5

<210> 84
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is pyroglutamic acid

<221> MOD_RES
<222> 5
<223> Alanine-therapeutic agent

<400> 84
Xaa Gly Arg Ala Xaa
1 5

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<210> 85
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is H-D-Ile

<221> MOD_RES
<222> 5
<223> Alanine- therapeutic agent

<400> 85
Xaa Pro Arg Ala Xaa
1 5

<210> 86
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is Cbo-L-(gamma)Glu(alpha-t-BuO):
Cbo is carbobenzoxy

<221> MOD_RES
<222> 5
<223> Alanine-therapeutic agent

<400> 86
Xaa Arg Ala Ala Xaa
1 5

<210> 87
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is H-D-Pro

<221> MOD_RES
<222> 5
<223> Alanine-therapeutic agent

<400> 87
Xaa Phe Arg Ala Xaa
1 5

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<210> 88
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is H-D-Val

<221> MUTAGEN
<222> 5
<223> Alanine-therapeutic agent

<400> 88
Xaa Leu Arg Ala Xaa
1 5

<210> 89
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is Bz-Ile:
Bz is benzoyl

<221> MOD_RES
<222> 6
<223> Alanine-therapeutic agent

<400> 89
Xaa Glu Gly Arg Ala Xaa
1 5

<210> 90
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is Bz-Ile:
Bz is benzoyl

<221> MOD_RES
<222> 6
<223> Alanine-therapeutic agent

<400> 90
Xaa Xaa Gly Arg Ala Xaa
1 5

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<210> 91
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is Benzoyl-Pro

<221> MOD_RES
<222> 5
<223> Alanine-therapeutic agent

<400> 91
Xaa Phe Arg Ala Xaa
1 5

<210> 92
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is H-D-Phe

<221> MOD_RES
<222> 2
<223> pipecolinic acid

<221> MOD_RES
<222> 5
<223> Alanine-therapeutic agent

<400> 92
Xaa Xaa Arg Ala Xaa
1 5

<210> 93
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is H-D-Val

<221> MOD_RES
<222> 5
<223> Alanine-therapeutic agent

<400> 93

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Xaa Leu Lys Ala Xaa
1 5

<210> 94
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is H-D-Nle

<221> MOD_RES
<222> 2
<223> HHT:
HHT is hexahydrotyrosyl

<221> MOD_RES
<222> 5
<223> Alanine-therapeutic agent

<400> 94
Xaa Xaa Lys Ala Xaa
1 5

<210> 95
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is pyroglutamic acid

<221> MOD_RES
<222> 7
<223> Alanine-therapeutic agent

<400> 95
Xaa Arg Thr Lys Arg Ala Xaa
1 5

<210> 96
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is H-Arg

<221> MOD_RES

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<222> 6
<223> Alanine-therapeutic agent

<400> 96
Xaa Gln Arg Arg Ala Xaa
1 5

<210> 97
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is Boc-Gln:
Boc is t-butoxycarbonyl

<221> MOD_RES
<222> 5
<223> Alanine-therapeutic agent

<400> 97
Xaa Gly Arg Ala Xaa
1 5

<210> 98
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is Z-Arg:
Z is benzyloxycarbonyl

<221> MOD_RES
<222> 4
<223> Alanine-therapeutic agent

<400> 98
Xaa Arg Ala Xaa
1

<210> 99
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is H-D-HHT: HHT is hexahydrotyrosol

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<221> MOD_RES
<222> 5
<223> Alanine-therapeutic agent

<400> 99
Xaa Ala Arg Ala Xaa
1 5

<210> 100
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is H-D-CHT:
HHT is hexahydrotyrosyl

<221> MOD_RES
<222> 5
<223> Alanine-therapeutic agent

<400> 100
Xaa Gly Arg Ala Xaa
1 5

<210> 101
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is MeSO₂-D-Phe

<221> MOD_RES
<222> 5
<223> Alanine-therapeutic agent

<400> 101
Xaa Pro Arg Ala Xaa
1 5

<210> 102
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1

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<223> Xaa is delta-Z-D-Lys: Z is benzyloxycarbonyl

<221> MOD_RES

<222> 5

<223> Alanine-therapeutic agent

<400> 102

Xaa Pro Arg Ala Xaa

1

5

<210> 103

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> MOD_RES

<222> 1

<223> Xaa is CH₃SO₂-D-CHA:
CHA is cyclohexylalanyl

<221> MOD_RES

<222> 2

<223> Xaa is But-Arg

<221> MOD_RES

<222> 4

<223> Alanine-therapeutic agent

<400> 103

Xaa Xaa Ala Xaa

1

<210> 104

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLTATION

<222> 1

<221> MOD_RES

<222> 6

<223> Alanine-therapeutic agent

<400> 104

Arg Gln Ser Arg Ala Xaa

1

5

<210> 105

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

-111-

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 7

<223> Ala-therapeutic agent

<400> 105

Arg Arg Gln Ser Arg Ala Xaa
1 5

<210> 106

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 8

<223> Alanine-therapeutic agent

<400> 106

Leu Arg Arg Gln Ser Arg Ala Xaa
1 5

<210> 107

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 5

<223> Alanine-therapeutic agent

<400> 107

Arg Gln Ser Arg Xaa
1 5

<210> 108

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> MOD_RES

<222> 1

<221> MOD_RES

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<222> 6
<223> Alanine-therapeutic agent

<400> 108
Arg Arg Gln Ser Arg Xaa
1 5

<210> 109
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Glycine-therapeutic agent

<400> 109
Leu Arg Arg Gln Ser Arg Gly Xaa
1 5

<210> 110
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> (0)...(0)

<221> MOD_RES
<222> 7
<223> Alanine-therapeutic agent

<400> 110
Leu Arg Arg Gln Ser Arg Xaa
1 5

<210> 111
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
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<221> ACETYLATION
<222> (0)...(0)

<221> MOD_RES
<222> 6
<223> Isoleucine-therapeutic agent

<400> 111

-113-

Arg Arg Gln Ser Arg Xaa
1 5

<210> 112
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Isoleucine-therapeutic agent

<400> 112
Leu Arg Arg Gln Ser Arg Ala Xaa
1 5

<210> 113
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> (1)...(0)

<221> MOD_RES
<222> 4
<223> Xaa is Quat: (R)-Glu(Alpha-(3-amidinobenzyl))

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic agent

<400> 113
Leu Arg Ala Xaa Gly Arg Ser Xaa
1 5

<210> 114
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 4
<223> Xaa is Quat: (R)-Glu(alpha-(3-amidinobenzyl))

<221> MOD_RES

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<222> 8
<223> Leucine-therapeutic agent

<400> 114
Leu Arg Ala Xaa Ala Arg Ser Xaa
1 5

<210> 115
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 4
<223> Xaa is Quat: (R)-Glu(alpha-(3-amidinobenzyl))

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic agent

<400> 115
Leu Arg Ser Xaa Gly Arg Ser Xaa
1 5

<210> 116
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 4
<223> Xaa is Quat: (R)-Glu(alpha-(3-amidinobenzyl))

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic agent

<400> 116
Leu Arg Ser Xaa Ala Arg Ser Xaa
1 5

<210> 117
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

-115-

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 8

<223> Leucine-therapeutic agent

<400> 117

Leu Arg Pro Arg Phe Lys Ser Xaa

1

5

<210> 118

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 7

<223> Leucine-therapeutic agent

<400> 118

Arg Pro Arg Phe Lys Ser Xaa

1

5

<210> 119

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 6

<223> Leucine-therapeutic agent

<400> 119

Pro Arg Phe Lys Ser Xaa

1

5

<210> 120

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

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<222> 8
<223> Leucine-therapeutic agent

<400> 120
Leu Arg Ser Lys Ser Arg Ser Xaa
1 5

<210> 121
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 121
Arg Ser Lys Ser Arg Ser Xaa
1 5

<210> 122
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 122
Ser Lys Ser Arg Ser Xaa
1 5

<210> 123
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic agent

<400> 123

-117-

Leu Arg Pro Arg Phe Arg Ser Xaa
1 5

<210> 124
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> (0)...(0)

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 124
Arg Pro Arg Phe Arg Ser Xaa
1 5

<210> 125
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 125
Pro Arg Phe Arg Ser Xaa
1 5

<210> 126
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> (0)...(0)

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic agent

<400> 126
Leu Arg Ser Arg Ser Arg Ser Xaa
1 5

<210> 127

-118-

<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 127
Arg Ser Arg Ser Arg Ser Xaa
1 5

<210> 128
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 128
Ser Arg Ser Arg Ser Xaa
1 5

<210> 129
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> (0)...(0)

<221> MOD_RES
<222> 4
<223> Xaa is Quat: (R)-Glu(alpha-(3-amidinobenzyl))

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic agent

<400> 129
Leu Arg Ala Xaa Gly Arg Ser Xaa
1 5

<210> 130

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<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 4
<223> Xaa is Quat: (R)-Glu(alpha-(3-amidinobenzyl))

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic agent

<400> 130
Leu Arg Ala Xaa Ala Arg Ser Xaa
1 5

<210> 131
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 4
<223> Xaa is Quat: (R)-Glu(alpha-(3-amidinobenzyl))

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic agent

<400> 131
Leu Arg Ser Xaa Gly Arg Ser Xaa
1 5

<210> 132
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 4
<223> Xaa is Quat: (R)-Glu(alpha-(3-amidinobenzyl))

<221> MOD_RES

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<222> 8
<223> Leucine-therapeutic agent

<400> 132
Leu Arg Ser Xaa Ala Arg Ser Xaa
1 5

<210> 133
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLTATION
<222> 1

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic agent

<400> 133
Leu Arg Pro Arg Phe Lys Ser Xaa
1 5

<210> 134
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLTATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 134
Arg Pro Arg Phe Lys Ser Xaa
1 5

<210> 135
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLTATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 135

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Pro Arg Phe Lys Ser Xaa

1 5

<210> 136

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 8

<223> Leucine-therapeutic agent

<400> 136

Leu Arg Ser Lys Ser Arg Ser Xaa

1 5

<210> 137

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 7

<223> Leucine-therapeutic agent

<400> 137

Arg Ser Lys Ser Arg Ser Xaa

1 5

<210> 138

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 6

<223> Leucine-therapeutic agent

<400> 138

Ser Lys Ser Arg Ser Xaa

1 5

<210> 139

-122-

<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic agent

<400> 139
Leu Arg Pro Arg Phe Arg Ser Xaa
1 5

<210> 140
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 140
Arg Pro Arg Phe Arg Ser Xaa
1 5

<210> 141
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 141
Pro Arg Phe Arg Ser Xaa
1 5

<210> 142
<211> 8
<212> PRT
<213> Artificial Sequence

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<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic agent

<400> 142
Leu Arg Ser Arg Ser Arg Ser Xaa
1 5

<210> 143
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 143
Arg Ser Arg Ser Arg Ser Xaa
1 5

<210> 144
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 144
Ser Arg Ser Arg Ser Xaa
1 5

<210> 145
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES

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<222> 1
<223> Xaa is pyroglutamic acid

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 145
Xaa Pro Arg Ser Xaa
1 5

<210> 146
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is CH₃SO₂-D-HHT;
HHT is hexahydrotyrosyl

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 146
Xaa Gly Arg Ser Xaa
1 5

<210> 147
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is n-p-tosyl-Gly

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 147
Xaa Pro Arg Ser Xaa
1 5

<210> 148
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> Conjugate

<221> MOD_RES

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<222> 1
<223> Xaa is Benzoyl-Val

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 148
Xaa Gly Arg Ser Xaa
1 5

<210> 149
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is CH₃SO₂-D-HHT;
HHT is hexahydrotyrosyl

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 149
Xaa Gly Arg Ser Xaa
1 5

<210> 150
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is N-alpha-Z-D-Arg;
Z is benzyloxycarbonyl

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 150
Xaa Gly Arg Ser Xaa
1 5

<210> 151
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

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<221> MOD_RES
<222> 1
<223> Xaa is pyroglutamic acid

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 151
Xaa Gly Arg Ser Xaa
1 5

<210> 152
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is H-D-Ile

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 152
Xaa Pro Arg Ser Xaa
1 5

<210> 153
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is Cbo-L-(gamma)Glu(alpha-t-BuO);
Cbo is carbobenzoxy

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 153
Xaa Gly Arg Ser Xaa
1 5

<210> 154
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

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<221> MOD_RES
<222> 1
<223> Xaa is H-D-Pro

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 154
Xaa Phe Arg Ser Xaa
1 5

<210> 155
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is H-D-Val

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 155
Xaa Leu Arg Ser Xaa
1 5

<210> 156
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is Bz-Ile;
Bz is benzoyl

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 156
Xaa Glu Gly Arg Ser Xaa
1 5

<210> 157
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

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<221> MOD_RES
<222> 1
<223> Xaa is Bz-Ile

<221> MOD_RES
<222> 2
<223> Xaa is Glu(gamma-OMe)

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 157
Xaa Xaa Gly Arg Ser Xaa
1 5

<210> 158
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is benzoyl-Pro

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 158
Xaa Phe Arg Ser Xaa
1 5

<210> 159
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is H-D-Phe

<221> MOD_RES
<222> 2
<223> Xaa is Pip is pipercolinic acid

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic acid

<400> 159
Xaa Xaa Arg Ser Xaa
1 5

<210> 160

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<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is H-D-Val

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic acid

<400> 160
Xaa Leu Lys Ser Xaa
1 5

<210> 161
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is H-D-Nle

<221> MOD_RES
<222> 2
<223> Xaa is HHT: hexahydrotyrosyl

<221> MOD_RES
<222> 5
<223> Xaa is leucine-therapeutic agent

<400> 161
Xaa Xaa Lys Ser Xaa
1 5

<210> 162
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is pyroglutamic acid

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 162
Xaa Arg Thr Lys Arg Ser Xaa

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1 5

<210> 163
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is H-Arg

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 163
Xaa Gln Arg Arg Ser Xaa
1 5

<210> 164
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is Boc-Gln

<221> MOD_RES
<222> 5
<223> Xaa is Leucine-therapeutic agent

<400> 164
Xaa Gly Arg Ser Xaa
1 5

<210> 165
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is Z-Arg:
Z is benzyloxycarbonyl

<221> MOD_RES
<222> 4
<223> Leucine-therapeutic agent

<400> 165
Xaa Arg Ser Xaa

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1

<210> 166
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is H-D-HHT: HHT is hexahydrotyrosyl

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 166
Xaa Ala Arg Ser Xaa
1 5

<210> 167
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is H-D-CHT: CHT is hexahydrotyrosyl

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 167
Xaa Gly Arg Ser Xaa
1 5

<210> 168
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is MeSO₂-dPhe

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 168
Xaa Pro Arg Ser Xaa
1 5

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<210> 169
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is delta-Z-D-Lys: Z is benzyloxycarbonyl

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 169
Xaa Pro Arg Ser Xaa
1 5

<210> 170
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is CH3SO2-D-CHA: CHA is cyclohexylalanyl

<221> MOD_RES
<222> 2
<223> Xaa is But-Arg

<221> MOD_RES
<222> 4
<223> Leucine-therapeutic agent

<400> 170
Xaa Xaa Ser Xaa
1

<210> 171
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 171

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Arg Gln Ser Arg Ser Xaa
1 5

<210> 172
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 172
Arg Arg Gln Ser Arg Ser Xaa
1 5

<210> 173
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic agent

<400> 173
Leu Arg Arg Gln Ser Arg Ser Xaa
1 5

<210> 174
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 174
Arg Gln Ser Arg Xaa
1 5

<210> 175

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<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 175
Arg Arg Gln Ser Arg Xaa
1 5

<210> 176
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic agent

<400> 176
Leu Arg Arg Gln Ser Arg Ser Xaa
1 5

<210> 177
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 177
Leu Arg Arg Gln Ser Arg Xaa
1 5

<210> 178
<211> 6
<212> PRT
<213> Artificial Sequence

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<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 178
Arg Arg Gln Ser Arg Xaa
1 5

<210> 179
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 9
<223> Leucine-therapeutic agent

<400> 179
Leu Arg Arg Gln Ser Arg Ser Xaa
1 5

<210> 180
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 180
Arg Gln Gly Arg Ser Xaa
1 5

<210> 181
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION

-136-

<222> 1

<221> MOD_RES

<222> 6

<223> Leucine-therapeutic agent

<400> 181

Arg Gln Ala Arg Ser Xaa
1 5

<210> 182

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 6

<223> Leucine-therapeutic agent

<400> 182

Arg Gln Phe Arg Ser Xaa
1 5

<210> 183

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 5

<223> Leucine-therapeutic agent

<400> 183

Arg Ser Arg Ser Xaa
1 5

<210> 184

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 5

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<223> Leucine-therapeutic agent

<400> 184

Arg Gly Arg Ser Xaa
1 5

<210> 185

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 5

<223> Leucine-therapeutic agent

<400> 185

Arg Ala Arg Ser Xaa
1 5

<210> 186

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 5

<223> Leucine-therapeutic agent

<400> 186

Arg Phe Arg Ser Xaa
1 5

<210> 187

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 5

<223> Leucine-therapeutic agent

<400> 187

Gln Ser Arg Ser Xaa

-138-

1 5

<210> 188
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 188
Gln Gly Arg Ser Xaa
1 5

<210> 189
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 189
Gln Ala Arg Ser Xaa
1 5

<210> 190
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 190
Gln Phe Arg Ser Xaa
1 5

<210> 191
<211> 9

-139-

<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 4
<223> Xaa is Quat: (R)-Glu(Alpha-(3-amidinobenzyl))

<221> MOD_RES
<222> 9
<223> Leucine-therapeutic agent

<400> 191
Leu Arg Ala Xaa Gly Arg Ser Ser Xaa
1 5

<210> 192
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 4
<223> Xaa is Quat: (R)-Glu(alpha-(3-amidinobenzyl))

<221> MOD_RES
<222> 9
<223> Leucine-therapeutic agent

<400> 192
Leu Arg Ala Xaa Ala Arg Ser Ser Xaa
1 5

<210> 193
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 4
<223> Xaa is Quat: (R)-Glu(alpha-(3-amidinobenzyl))

<221> MOD_RES
<222> 9

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<223> Leucine-therapeutic agent

<400> 193

Leu Arg Ser Xaa Gly Arg Ser Ser Xaa
1 5

<210> 194

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 4

<223> Xaa is Quat: (R)-Glu(alpha-(3-amidinobenzyl))

<221> MOD_RES

<222> 9

<223> Leucine-therapeutic agent

<400> 194

Leu Arg Ser Xaa Ala Arg Ser Ser Xaa
1 5

<210> 195

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 9

<223> Leucine-therapeutic agent

<400> 195

Leu Arg Pro Arg Phe Lys Ser Ser Xaa
1 5

<210> 196

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 8

-141-

<223> Leucine-therapeutic agent

<400> 196

Arg Pro Arg Phe Lys Ser Ser Xaa
1 5

<210> 197

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 7

<223> Leucine-therapeutic agent

<400> 197

Pro Arg Phe Lys Ser Ser Xaa
1 5

<210> 198

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 9

<223> Leucine-therapeutic agent

<400> 198

Leu Arg Ser Lys Ser Arg Ser Ser Xaa
1 5

<210> 199

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 8

<223> Leucine-therapeutic agent

<400> 199

Arg Ser Lys Ser Arg Ser Ser Xaa

-142-

1 5

<210> 200
<211> 7
<212> PRT
<213> Aritificial sequence

<220>
<223> Conjugate

<221> ACETYLTATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 200
Ser Lys Ser Arg Ser Ser Xaa
1 5

<210> 201
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLTATION
<222> 1

<221> MOD_RES
<222> 9
<223> Leucine-therapeutic agent

<400> 201
Leu Arg Pro Arg Phe Arg Ser Ser Xaa
1 5

<210> 202
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLTATION
<222> 1

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic agent

<400> 202
Arg Pro Arg Phe Arg Ser Ser Xaa
1 5

<210> 203
<211> 7

-143-

<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 203
Pro Arg Phe Arg Ser Ser Xaa
1 5

<210> 204
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 9
<223> Leucine-therapeutic agent

<400> 204
Leu Arg Ser Arg Ser Arg Ser Ser Xaa
1 5

<210> 205
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic agent

<400> 205
Arg Ser Arg Ser Arg Ser Ser Xaa
1 5

<210> 206
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

-144-

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 7

<223> Leucine-therapeutic agent

<400> 206

Ser Arg Ser Arg Ser Ser Xaa
1 5

<210> 207

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> (0)...(0)

<221> MOD_RES

<222> 4

<223> Xaa is Quat: (R)-Glu(alpha-(3-amidinobenzyl))

<221> MOD_RES

<222> 9

<223> Leucine-therapeutic agent

<400> 207

Leu Arg Ala Xaa Gly Arg Ser Ser Xaa
1 5

<210> 208

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 4

<223> Xaa is Quat: (R)-Glu(alpha-(3-amidinobenzyl))

<221> MOD_RES

<222> 9

<223> Leucine-therapeutic agent

<400> 208

Leu Arg Ala Xaa Ala Arg Ser Ser Xaa
1 5

<210> 209

<211> 9

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<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 4
<223> Xaa is Quat: (R)-Glu(alpha-(3-amidinobenzyl))

<221> MOD_RES
<222> 9
<223> Leucine-therapeutic agent

<400> 209
Leu Arg Ser Xaa Gly Arg Ser Ser Xaa
1 5

<210> 210
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 4
<223> Xaa is Quat: (R)-Glu(alpha-(3-amidinobenzyl))

<221> MOD_RES
<222> 9
<223> Leucine-therapeutic agent

<400> 210
Leu Arg Ser Xaa Ala Arg Ser Ser Xaa
1 5

<210> 211
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 9
<223> Leucine-therapeutic agent

<400> 211
Leu Arg Pro Arg Phe Lys Ser Ser Xaa

-146-

1 5

<210> 212
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 9
<223> Leucine-therapeutic agent

<400> 212
Arg Pro Arg Phe Lys Ser Ser Xaa
1 5

<210> 213
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 213
Pro Arg Phe Lys Ser Ser Xaa
1 5

<210> 214
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 9
<223> Leucine-therapeutic agent

<400> 214
Leu Arg Ser Lys Ser Arg Ser Ser Xaa
1 5

<210> 215
<211> 8

-147-

<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic agent

<400> 215
Arg Ser Lys Ser Arg Ser Ser Xaa
1 5

<210> 216
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 216
Ser Lys Ser Arg Ser Ser Xaa
1 5

<210> 217
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 9
<223> Leucine-therapeutic agent

<400> 217
Leu Arg Pro Arg Phe Arg Ser Ser Xaa
1 5

<210> 218
<211> 8
<212> PRT
<213> Artificial Sequence

<220>

-148-

<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic agent

<400> 218
Arg Pro Arg Phe Arg Ser Ser Xaa
1 5

<210> 219
<211> 7
<212> PRT
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<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 219
Pro Arg Phe Arg Ser Ser Xaa
1 5

<210> 220
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 9
<223> Leucine-therapeutic agent

<400> 220
Leu Arg Ser Arg Ser Arg Ser Ser Xaa
1 5

<210> 221
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

-149-

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic agent

<400> 221
Arg Ser Arg Ser Arg Ser Ser Xaa
1 5

<210> 222
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLTATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 222
Ser Arg Ser Arg Ser Ser Xaa
1 5

<210> 223
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is pyroglutamic acid

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 223
Xaa Pro Arg Ser Ser Xaa
1 5

<210> 224
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is CH3SO2-D-HHT;
HHT is hexahydrotyrosyl

<221> MOD_RES

-150-

<222> 6
<223> Leucine-therapeutic agent

<400> 224
Xaa Gly Arg Ser Ser Xaa
1 5

<210> 225
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is n-p-tosyl-Gly

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 225
Xaa Pro Arg Ser Ser Xaa
1 5

<210> 226
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is Benzoyl-Val

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 226
Xaa Gly Arg Ser Ser Xaa
1 5

<210> 227
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is CH₃SO₂-D-HHT;
HHT is hexahydrotyrosyl

<221> MOD_RES

-151-

<222> 6
<223> Leucine-therapeutic agent

<400> 227
Xaa Gly Arg Ser Ser Xaa
1 5

<210> 228
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is N-alpha-Z-D-Arg;
Z is benzyloxycarbonyl

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 228
Xaa Gly Arg Ser Ser Xaa
1 5

<210> 229
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is pyroglutamic acid

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 229
Xaa Gly Arg Ser Ser Xaa
1 5

<210> 230
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is H-D-Ile

<221> MOD_RES

-152-

<222> 6
<223> Leucine-therapeutic agent

<400> 230
Xaa Pro Arg Ser Ser Xaa
1 5

<210> 231
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is Cbo-L-(gamma)Glu(alpha-t-BuO);
Cbo is carbobenzoxy

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 231
Xaa Gly Arg Ser Ser Xaa
1 5

<210> 232
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is H-D-Pro

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 232
Xaa Phe Arg Ser Ser Xaa
1 5

<210> 233
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is H-D-Val

<221> MOD_RES

-153-

<222> 6
<223> Leucine-therapeutic agent

<400> 233
Xaa Leu Arg Ser Ser Xaa
1 5

<210> 234
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is Bz-Ile;
Bz is benzoyl

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 234
Xaa Glu Gly Arg Ser Ser Xaa
1 5

<210> 235
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is Bz-Ile

<221> MOD_RES
<222> 2
<223> Xaa is Glu(gamma-OMe)

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 235
Xaa Xaa Gly Arg Ser Ser Xaa
1 5

<210> 236
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES

-154-

<222> 1
<223> Xaa is benzoyl-Pro

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 236
Xaa Phe Arg Ser Ser Xaa
1 5

<210> 237
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is H-D-Phe

<221> MOD_RES
<222> 2
<223> Xaa is Pip is pipecolinic acid

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic acid

<400> 237
Xaa Xaa Arg Ser Ser Xaa
1 5

<210> 238
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is H-D-Val

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic acid

<400> 238
Xaa Leu Lys Ser Ser Xaa
1 5

<210> 239
<211> 6
<212> PRT
<213> Artificial Sequence

<220>

-155-

<223> Conjugate

<221> MOD_RES

<222> 1

<223> Xaa is H-D-Nle

<221> MOD_RES

<222> 2

<223> Xaa is HHT: hexahydrotyrosyl

<221> MOD_RES

<222> 6

<223> Xaa is leucine-therapeutic agent

<400> 239

Xaa Xaa Lys Ser Ser Xaa

1

5

<210> 240

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> MOD_RES

<222> 1

<223> Xaa is pyroglutamic acid

<221> MOD_RES

<222> 8

<223> Leucine-therapeutic agent

<400> 240

Xaa Arg Thr Lys Arg Ser Ser Xaa

1

5

<210> 241

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> MOD_RES

<222> 1

<223> Xaa is H-Arg

<221> MOD_RES

<222> 7

<223> Leucine-therapeutic agent

<400> 241

Xaa Gln Arg Arg Ser Ser Xaa

1

5

<210> 242

<211> 6

<212> PRT

-156-

<213> Artificial Sequence

<220>

<223> Conjugate

<221> MOD_RES

<222> 1

<223> Xaa is Boc-Gln

<221> MOD_RES

<222> 6

<223> Xaa is Leucine-therapeutic agent

<400> 242

Xaa Gly Arg Ser Ser Xaa

1

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<210> 243

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> MOD_RES

<222> 1

<223> Xaa is Z-Arg:

Z is benzyloxycarbonyl

<221> MOD_RES

<222> 5

<223> Leucine-therapeutic agent

<400> 243

Xaa Arg Ser Ser Xaa

1

5

<210> 244

<211> 6

<212> PRT

<213> Artificial Sequence

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<223> Conjugate

<221> MOD_RES

<222> 1

<223> Xaa is H-D-HHT: HHT is hexahydrotyrosyl

<221> MOD_RES

<222> 6

<223> Leucine-therapeutic agent

<400> 244

Xaa Ala Arg Ser Ser Xaa

1

5

<210> 245

<211> 6

<212> PRT

-157-

<213> Artificial Sequence

<220>

<223> Conjugate

<221> MOD_RES

<222> 1

<223> Xaa is H-D-CHT: CHT is hexahydrotyrosyl

<221> MOD_RES

<222> 6

<223> Leucine-therapeutic agent

<400> 245

Xaa Gly Arg Ser Ser Xaa

1

5

<210> 246

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> MOD_RES

<222> 1

<223> Xaa is MeSO₂-dPhe

<221> MOD_RES

<222> 6

<223> Leucine-therapeutic agent

<400> 246

Xaa Pro Arg Ser Ser Xaa

1

5

<210> 247

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> MOD_RES

<222> 1

<223> Xaa is delta-Z-D-Lys: Z is benzyloxycarbonyl

<221> MOD_RES

<222> 6

<223> Leucine-therapeutic agent

<400> 247

Xaa Pro Arg Ser Ser Xaa

1

5

<210> 248

<211> 5

<212> PRT

<213> Artificial Sequence

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<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is CH3SO2-D-CHA: CHA is cyclohexylalanyl

<221> MOD_RES
<222> 2
<223> Xaa is But-Arg

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 248
Xaa Xaa Ser Ser Xaa
1 5

<210> 249
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 249
Arg Gln Ser Arg Ser Ser Xaa
1 5

<210> 250
<211> 8
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<220>
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<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic agent

<400> 250
Arg Arg Gln Ser Arg Ser Ser Xaa
1 5

<210> 251
<211> 9
<212> PRT

-159-

<213> Artificial sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 9
<223> Leucine-therapeutic agent

<400> 251
Leu Arg Arg Gln Ser Arg Ser Ser Xaa
1 5

<210> 252
<211> 5
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<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 252
Arg Gln Ser Arg Xaa
1 5

<210> 253
<211> 6
<212> PRT
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<220>
<223> Conjugate

<221> ACETYLATION
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<221> MOD_RES
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<400> 253
Arg Arg Gln Ser Arg Xaa
1 5

<210> 254
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

-160-

<221> MOD_RES
<222> 1

<221> MOD_RES
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<400> 254
Leu Arg Arg Gln Ser Arg Ser Ser Xaa
1 5

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<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic agent

<400> 255
Leu Arg Arg Gln Ser Arg Ser Xaa
1 5

<210> 256
<211> 7
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<221> ACETYLATION
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<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 256
Arg Arg Gln Ser Arg Ser Xaa
1 5

<210> 257
<211> 9
<212> PRT
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<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES

-161-

<222> 9
<223> Leucine-therapeutic agent

<400> 257
Leu Arg Arg Gln Ser Arg Ser Ser Xaa
1 5

<210> 258
<211> 7
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<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 258
Arg Gln Gly Arg Ser Ser Xaa
1 5

<210> 259
<211> 7
<212> PRT
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<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 259
Arg Gln Ala Arg Ser Ser Xaa
1 5

<210> 260
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<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic acid

<400> 260

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Arg Gln Phe Arg Ser Ser Xaa
1 5

<210> 261
<211> 6
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<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 261
Arg Ser Arg Ser Ser Xaa
1 5

<210> 262
<211> 6
<212> PRT
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<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 262
Arg Gly Arg Ser Ser Xaa
1 5

<210> 263
<211> 6
<212> PRT
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<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 263
Arg Ala Arg Ser Ser Xaa
1 5

<210> 264

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<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
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<400> 264
Arg Phe Arg Ser Ser Xaa
1 5

<210> 265
<211> 6
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<223> Conjugate

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<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 265
Gln Ser Arg Ser Ser Xaa
1 5

<210> 266
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<223> Conjugate

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<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 266
Gln Gly Arg Ser Ser Xaa
1 5

<210> 267
<211> 6
<212> PRT
<213> Artificial Sequence

-164-

<220>
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<221> ACETYLTATION
<222> 1

<221> MOD_RES
<222> 6
<223> leucine-therapeutic agent

<400> 267
Gln Ala Arg Ser Ser Xaa
1 5

<210> 268
<211> 6
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<222> 6
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<400> 268
Gln Phe Arg Ser Ser Xaa
1 5

<210> 269
<211> 816
<212> DNA
<213> Homo Sapien

<220>
<221> CDS
<222> (1)...(816)
<223> Nucleotide sequence encoding MTSP25, including
MTSP25 protease domain

<221> misc feature
<222> (248)...(270)
<223> Transmembrane domain encompasses amino acids
248-270 at the C-terminus of the trypsin-like
serine protease domain (amino acids 1-237)

<400> 269
att ata ggg ggc acc gaa gca caa gct ggc gca tgg ccg tgg gtg gtg 48
Ile Ile Gly Gly Thr Glu Ala Gln Ala Gly Ala Trp Pro Trp Val Val
1 5 10 15
agc ctg cag att aaa tat ggc cgt gtt ctt gtt cat gta tgt ggg gga 96
Ser Leu Gln Ile Lys Tyr Gly Arg Val Leu Val His Val Cys Gly Gly
20 25 30
acc cta gtg aga gag agg tgg gtc ctc aca gct gcc cac tgc act aaa 144
Thr Leu Val Arg Glu Arg Trp Val Leu Thr Ala Ala His Cys Thr Lys

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35	40	45	
gac gct agc gat cct tta atg tgg aca gct gtg att gga act aat aat Asp Ala Ser Asp Pro Leu Met Trp Thr Ala Val Ile Gly Thr Asn Asn 50 55 60			192
ata cat gga cgc tat cct cat acc aag aag ata aaa att aaa gca atc Ile His Gly Arg Tyr Pro His Thr Lys Lys Ile Lys Ile Lys Ala Ile 65 70 75 80			240
att att cat cca aac ttc att ttg gaa tct tat gta aat gat att gca Ile Ile His Pro Asn Phe Ile Leu Glu Ser Tyr Val Asn Asp Ile Ala 85 90 95			288
ctt ttt cac tta aaa aaa gca gtg agg tat aat gac tat att cag cct Leu Phe His Leu Lys Lys Ala Val Arg Tyr Asn Asp Tyr Ile Gln Pro 100 105 110			336
att tgc cta cct ttt gat gtt ttc caa atc ctg gac gga aac aca aag Ile Cys Leu Pro Phe Asp Val Phe Gln Ile Leu Asp Gly Asn Thr Lys 115 120 125			384
tgt ttt ata agt ggc tgg gga aga aca aaa gaa gaa ggt aac gct aca Cys Phe Ile Ser Gly Trp Ala Arg Thr Lys Glu Glu Gly Asn Ala Thr 130 135 140			432
aat att tta caa gat gca gaa gtg cat tat att tct cga gag atg tgt Asn Ile Leu Gln Asp Ala Glu Val His Tyr Ile Ser Arg Glu Met Cys 145 150 155 160			480
aat tct gag agg agt tat ggg gga ata att cct aac act tca ttt tgt Asn Ser Glu Arg Ser Tyr Gly Gly Ile Ile Pro Asn Thr Ser Phe Cys 165 170 175			528
gca ggt gat gaa gat gga gct ttt gat act tgc agg ggt gac agt ggg Ala Gly Asp Glu Asp Gly Ala Phe Asp Thr Cys Arg Gly Asp Ser Gly 180 185 190			576
gga cca tta atg tgc tac tta cca gaa tat aaa aga ttt ttt gta atg Gly Pro Leu Met Cys Tyr Leu Pro Glu Tyr Lys Arg Phe Phe Val Met 195 200 205			624
gga att acc agt tac gga cat ggc tgt ggt cga aga ggt ttt cct ggt Gly Ile Thr Ser Tyr Gly His Gly Cys Gly Arg Arg Gly Phe Pro Gly 210 215 220			672
gtc tat att ggg cca tcc ttc tac caa aag tgg ctg aca gag cat ttc Val Tyr Ile Gly Pro Ser Phe Tyr Gln Lys Trp Leu Thr Glu His Phe 225 230 235 240			720
ttc cat gca agc act caa ggc ata ctt act ata aat att tta cgt ggc Phe His Ala Ser Thr Gln Gly Ile Leu Thr Ile Asn Ile Leu Arg Gly 245 250 255			768
cag atc ctc ata gct tta tgt ttt gtc atc tta cta gca aca aca taa Gln Ile Leu Ile Ala Leu Cys Phe Val Ile Leu Leu Ala Thr Thr * 260 265 270			816

<210> 270

<211> 271

<212> PRT

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<213> Homo Sapien

<400> 270

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Ile Ile Gly Gly Thr Glu Ala Gln Ala Gly Ala Trp Pro Trp Val Val
 1           5           10           15
Ser Leu Gln Ile Lys Tyr Gly Arg Val Leu Val His Val Cys Gly Gly
 20           25           30
Thr Leu Val Arg Glu Arg Trp Val Leu Thr Ala Ala His Cys Thr Lys
 35           40           45
Asp Ala Ser Asp Pro Leu Met Trp Thr Ala Val Ile Gly Thr Asn Asn
 50           55           60
Ile His Gly Arg Tyr Pro His Thr Lys Lys Ile Lys Ile Lys Ala Ile
 65           70           75           80
Ile Ile His Pro Asn Phe Ile Leu Glu Ser Tyr Val Asn Asp Ile Ala
 85           90           95
Leu Phe His Leu Lys Lys Ala Val Arg Tyr Asn Asp Tyr Ile Gln Pro
 100          105          110
Ile Cys Leu Pro Phe Asp Val Phe Gln Ile Leu Asp Gly Asn Thr Lys
 115          120          125
Cys Phe Ile Ser Gly Trp Gly Arg Thr Lys Glu Glu Gly Asn Ala Thr
 130          135          140
Asn Ile Leu Gln Asp Ala Glu Val His Tyr Ile Ser Arg Glu Met Cys
 145          150          155          160
Asn Ser Glu Arg Ser Tyr Gly Gly Ile Ile Pro Asn Thr Ser Phe Cys
 165          170          175
Ala Gly Asp Glu Asp Gly Ala Phe Asp Thr Cys Arg Gly Asp Ser Gly
 180          185          190
Gly Pro Leu Met Cys Tyr Leu Pro Glu Tyr Lys Arg Phe Phe Val Met
 195          200          205
Gly Ile Thr Ser Tyr Gly His Gly Cys Gly Arg Arg Gly Phe Pro Gly
 210          215          220
Val Tyr Ile Gly Pro Ser Phe Tyr Gln Lys Trp Leu Thr Glu His Phe
 225          230          235          240
Phe His Ala Ser Thr Gln Gly Ile Leu Thr Ile Asn Ile Leu Arg Gly
 245          250          255
Gln Ile Leu Ile Ala Leu Cys Phe Val Ile Leu Leu Ala Thr Thr
 260          265          270

```

<210> 271

<211> 8

<212> PRT

<213> amino acids 401-407 of SEQ ID No. 97 in WO 02/00860

<400> 271

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Arg Lys His Leu Pro Arg Pro Ala
 1           5

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<210> 272

<211> 228

<212> PRT

<213> alternative PD1 of MTSP12

<400> 272

```

Ile Val Gly Gly Met Glu Ala Ser Pro Gly Glu Phe Pro Trp Gln Ala
 1           5           10           15
Ser Leu Arg Glu Asn Lys Glu His Phe Cys Gly Ala Ala Ile Ile Asn
 20           25           30
Ala Arg Trp Leu Val Ser Ala Ala His Cys Phe Asn Glu Phe Gln Asp
 35           40           45

```

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```

Pro Thr Lys Trp Val Ala Tyr Val Gly Ala Thr Tyr Leu Ser Gly Ser
 50      55      60
Glu Ala Ser Thr Val Arg Ala Gln Val Val Gln Ile Val Lys His Pro
65      70      75      80
Leu Tyr Asn Ala Asp Thr Ala Asp Phe Asp Val Ala Val Leu Glu Leu
      85      90      95
Thr Ser Pro Leu Pro Phe Gly Arg His Ile Gln Pro Val Cys Leu Pro
      100      105      110
Ala Ala Thr His Ile Phe Pro Pro Ser Lys Lys Cys Leu Ile Ser Gly
      115      120      125
Trp Gly Tyr Leu Lys Glu Asp Phe Leu Arg Lys His Leu Pro Arg Pro
      130      135      140
Ala Val Lys Pro Gly Val Leu Gln Lys Ala Thr Val Glu Leu Leu Asp
145      150      155      160
Gln Ala Leu Cys Ala Ser Leu Tyr Gly His Ser Leu Thr Asp Arg Met
      165      170      175
Val Cys Ala Gly Tyr Leu Asp Gly Lys Val Asp Ser Cys Gln Gly Asp
      180      185      190
Ser Gly Gly Pro Leu Val Cys Glu Glu Pro Ser Gly Arg Phe Ser Leu
      195      200      205
Ala Gly Ile Val Ser Trp Gly Ile Gly Cys Ala Glu Ala Arg Arg Pro
      210      215      220
Gly Val Tyr Ala
225

```

<210> 273

<211> 804

<212> DNA

<213> Homo Sapien

<220>

<221> CDS

<222> (1)...(804)

<223> Nucleotide sequence encoding MTSP20, including
MTSP20 protease domain

<400> 273

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aca gca ggt ccc cag gca gga gca ccc tcc cca tgg ccc tgg gag gcc      48
Thr Ala Gly Pro Gln Ala Gly Ala Pro Ser Pro Trp Pro Trp Glu Ala
 1      5      10      15

agg ctg atg cac cag gga cag ctg gcc tgt ggc gga gcc ctg gtg tca      96
Arg Leu Met His Gln Gly Gln Leu Ala Cys Gly Gly Ala Leu Val Ser
      20      25      30

gag gag acg gtg cta act gtt gcc cac tgc ttc att ggg cgc cag gcc      144
Glu Glu Thr Val Leu Thr Val Ala His Cys Phe Ile Gly Arg Gln Ala
      35      40      45

cca gag gaa tgg agc gta ggg ctg ggg acc aga ccg gag gag tgg ggc      192
Pro Glu Glu Trp Ser Val Gly Leu Gly Thr Arg Pro Glu Glu Trp Gly
      50      55      60

ctg aag cag ctc atc ctg cat gga gcc tac acc cac cct gag ggg ggc      240
Leu Lys Gln Leu Ile Leu His Gly Ala Tyr Thr His Pro Glu Gly Gly
      65      70      75      80

tac gac atg gcc ctc ctg ctg ctg gcc cag oct gtg aca ctg gga gcc      288
Tyr Asp Met Ala Leu Leu Leu Leu Ala Gln Pro Val Thr Leu Gly Ala
      85      90      95

```

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agc ctg cgg ccc ctc tgc ctg ccc tat cct gac cac cac ctg cct gat 336
 Ser Leu Arg Pro Leu Cys Leu Pro Tyr Pro Asp His His Leu Pro Asp
 100 105 110

ggg gag cgt ggc tgg gtt ctg gga cgg gcc cgc cca gga gca ggc atc 384
 Gly Glu Arg Gly Trp Val Leu Gly Arg Ala Arg Pro Gly Ala Gly Ile
 115 120 125

agc tcc ctc cag aca gtg ccc gtg acc ctc ctg ggg cct agg gcc tgc 432
 Ser Ser Leu Gln Thr Val Pro Val Thr Leu Leu Gly Pro Arg Ala Cys
 130 135 140

agc cgg ctg cat gca gct cct ggg ggt gat ggc agc cct att ctg ccg 480
 Ser Arg Leu His Ala Pro Gly Gly Asp Gly Ser Pro Ile Leu Pro
 145 150 155 160

ggg atg gtg tgt acc agt gct gtg ggt gag ctg ccc agc tgt gag ggc 528
 Gly Met Val Cys Thr Ser Ala Val Gly Glu Leu Pro Ser Cys Glu Gly
 165 170 175

ctg tct ggg gca cca ctg gtg cat gag gtg agg ggc aca tgg ttc ctg 576
 Leu Ser Gly Ala Pro Leu Val His Glu Val Arg Gly Thr Trp Phe Leu
 180 185 190

gcc ggg ctg cac agc ttc gga gat gct tgc caa ggc ccc gcc agg ccg 624
 Ala Gly Leu His Ser Phe Gly Asp Ala Cys Gln Gly Pro Ala Arg Pro
 195 200 205

gcg gtc ttc acc gcg ctc cct gcc tat gag gac tgg gtc agc agt ttg 672
 Ala Val Phe Thr Ala Leu Pro Ala Tyr Glu Asp Trp Val Ser Ser Leu
 210 215 220

gac tgg cag gtc tac ttc gcc gag gaa cca gag ccc gag gct gag cct 720
 Asp Trp Gln Val Tyr Phe Ala Glu Glu Pro Glu Pro Glu Ala Glu Pro
 225 230 235 240

gga agc tgc ctg gcc aac atg agt atg tgg ccc cgg ggc ctc ctg cca 768
 Gly Ser Cys Leu Ala Asn Met Ser Met Trp Pro Arg Gly Leu Leu Pro
 245 250 255

aac cct gcc tct cca gga ccc ttc tct ctc cag tga 804
 Asn Pro Ala Ser Pro Gly Pro Phe Ser Leu Gln *
 260 265

<210> 274
 <211> 267
 <212> PRT
 <213> Homo Sapien

<400> 274
 Thr Ala Gly Pro Gln Ala Gly Ala Pro Ser Pro Trp Pro Trp Glu Ala
 1 5 10 15
 Arg Leu Met His Gln Gly Gln Leu Ala Cys Gly Gly Ala Leu Val Ser
 20 25 30
 Glu Glu Thr Val Leu Thr Val Ala His Cys Phe Ile Gly Arg Gln Ala
 35 40 45
 Pro Glu Glu Trp Ser Val Gly Leu Gly Thr Arg Pro Glu Glu Trp Gly
 50 55 60
 Leu Lys Gln Leu Ile Leu His Gly Ala Tyr Thr His Pro Glu Gly Gly
 65 70 75 80

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Tyr Asp Met Ala Leu Leu Leu Leu Ala Gln Pro Val Thr Leu Gly Ala
 85 90 95
 Ser Leu Arg Pro Leu Cys Leu Pro Tyr Pro Asp His His Leu Pro Asp
 100 105 110
 Gly Glu Arg Gly Trp Val Leu Gly Arg Ala Arg Pro Gly Ala Gly Ile
 115 120 125
 Ser Ser Leu Gln Thr Val Pro Val Thr Leu Leu Gly Pro Arg Ala Cys
 130 135 140
 Ser Arg Leu His Ala Ala Pro Gly Gly Asp Gly Ser Pro Ile Leu Pro
 145 150 155 160
 Gly Met Val Cys Thr Ser Ala Val Gly Glu Leu Pro Ser Cys Glu Gly
 165 170 175
 Leu Ser Gly Ala Pro Leu Val His Glu Val Arg Gly Thr Trp Phe Leu
 180 185 190
 Ala Gly Leu His Ser Phe Gly Asp Ala Cys Gln Gly Pro Ala Arg Pro
 195 200 205
 Ala Val Phe Thr Ala Leu Pro Ala Tyr Glu Asp Trp Val Ser Ser Leu
 210 215 220
 Asp Trp Gln Val Tyr Phe Ala Glu Glu Pro Glu Pro Glu Ala Glu Pro
 225 230 235 240
 Gly Ser Cys Leu Ala Asn Met Ser Met Trp Pro Arg Gly Leu Leu Pro
 245 250 255
 Asn Pro Ala Ser Pro Gly Pro Phe Ser Leu Gln
 260 265

<210> 275

<211> 699

<212> DNA

<213> Homo Sapien

<220>

<221> CDS

<222> (1)...(699)

 <223> Nucleotide sequence encoding MTSP22, including
 MTSP22 protease domain

<400> 275

att gtg aat gga aaa agc tcc ctg gag ggg gca tgg cca tgg cag gcc	48
Ile Val Asn Gly Lys Ser Ser Leu Glu Gly Ala Trp Pro Trp Gln Ala	
1 5 10 15	
agc atg caa tgg aaa ggc cgt cac tac tgt gga gcc tct ctg atc agc	96
Ser Met Gln Trp Lys Gly Arg His Tyr Cys Gly Ala Ser Leu Ile Ser	
20 25 30	
agc agg tgg cta tta tct gca gct cac tgc ttt gct aag aaa aat aat	144
Ser Arg Trp Leu Leu Ser Ala Ala His Cys Phe Ala Lys Lys Asn Asn	
35 40 45	
tca aaa gat tgg act gtc aac ttt gga gtt gta gta aat aaa cca tat	192
Ser Lys Asp Trp Thr Val Asn Phe Gly Val Val Val Asn Lys Pro Tyr	
50 55 60	
atg aca cgg aaa gtc caa aac att att ttt cat gaa aat tat agc agt	240
Met Thr Arg Lys Val Gln Asn Ile Ile Phe His Glu Asn Tyr Ser Ser	
65 70 75 80	
cct ggg ctt cat gat gat att gcc ctt gtg cag ctt gct gaa gaa gtt	288
Pro Gly Leu His Asp Asp Ile Ala Leu Val Gln Leu Ala Glu Glu Val	
85 90 95	

-170-

tct ttt aca gag tac att cgt aag att tgt ctt cct gaa gcc aaa atg 336
 Ser Phe Thr Glu Tyr Ile Arg Lys Ile Cys Leu Pro Glu Ala Lys Met
 100 105 110

aag ctc tca gaa aat gac aat gtt gta gtt aca ggt tgg gga aca ctt 384
 Lys Leu Ser Glu Asn Asp Asn Val Val Val Thr Gly Trp Gly Thr Leu
 115 120 125

tat atg aat ggt tca ttt cca gtg ata ctt caa gaa gcc ttt ttg aag 432
 Tyr Met Asn Gly Ser Phe Pro Val Ile Leu Gln Glu Ala Phe Leu Lys
 130 135 140

att att gac aac aaa att tgc aat gcc tca tat gca tac tct ggc tta 480
 Ile Ile Asp Asn Lys Ile Cys Asn Ala Ser Tyr Ala Tyr Ser Gly Leu
 145 150 155 160

gtg act gat aca atg tta tgt gct gga ttt atg tca gga gaa gct gat 528
 Val Thr Asp Thr Met Leu Cys Ala Gly Phe Met Ser Gly Glu Ala Asp
 165 170 175

gca tgt cag aat gat tct ggt gga cca cta gct tac cct gat tcc aga 576
 Ala Cys Gln Asn Asp Ser Gly Gly Pro Leu Ala Tyr Pro Asp Ser Arg
 180 185 190

aat atc tgg cat ctt gtt gga ata gta agc tgg ggt gat gga tgt ggt 624
 Asn Ile Trp His Leu Val Gly Ile Val Ser Trp Gly Asp Gly Cys Gly
 195 200 205

aaa aag aat aag cca ggt gtc tat act cga gtg act tct tat cgc aat 672
 Lys Lys Asn Lys Pro Gly Val Tyr Thr Arg Val Thr Ser Tyr Arg Asn
 210 215 220

tgg att aca tcc aag act gga ctc tga 699
 Trp Ile Thr Ser Lys Thr Gly Leu *
 225 230

<210> 276

<211> 232

<212> PRT

<213> Homo Sapien

<400> 276

Ile Val Asn Gly Lys Ser Ser Leu Glu Gly Ala Trp Pro Trp Gln Ala
 1 5 10 15
 Ser Met Gln Trp Lys Gly Arg His Tyr Cys Gly Ala Ser Leu Ile Ser
 20 25 30
 Ser Arg Trp Leu Leu Ser Ala Ala His Cys Phe Ala Lys Lys Asn Asn
 35 40 45
 Ser Lys Asp Trp Thr Val Asn Phe Gly Val Val Val Asn Lys Pro Tyr
 50 55 60
 Met Thr Arg Lys Val Gln Asn Ile Ile Phe His Glu Asn Tyr Ser Ser
 65 70 75 80
 Pro Gly Leu His Asp Asp Ile Ala Leu Val Gln Leu Ala Glu Glu Val
 85 90 95
 Ser Phe Thr Glu Tyr Ile Arg Lys Ile Cys Leu Pro Glu Ala Lys Met
 100 105 110
 Lys Leu Ser Glu Asn Asp Asn Val Val Val Thr Gly Trp Gly Thr Leu
 115 120 125
 Tyr Met Asn Gly Ser Phe Pro Val Ile Leu Gln Glu Ala Phe Leu Lys
 130 135 140

-171-

```

Ile Ile Asp Asn Lys Ile Cys Asn Ala Ser Tyr Ala Tyr Ser Gly Leu
145          150          155          160
Val Thr Asp Thr Met Leu Cys Ala Gly Phe Met Ser Gly Glu Ala Asp
          165          170          175
Ala Cys Gln Asn Asp Ser Gly Gly Pro Leu Ala Tyr Pro Asp Ser Arg
          180          185          190
Asn Ile Trp His Leu Val Gly Ile Val Ser Trp Gly Asp Gly Cys Gly
          195          200          205
Lys Lys Asn Lys Pro Gly Val Tyr Thr Arg Val Thr Ser Tyr Arg Asn
          210          215          220
Trp Ile Thr Ser Lys Thr Gly Leu

```

```

<210> 277
<211> 6
<212> PRT
<213> Artificial Sequence

```

```

<220>
<221> ACETYLTATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<223> conjugate

```

```

<400> 277
Gly Ser Gly Arg Ser Xaa
1          5

```

```

<210> 278
<211> 6
<212> PRT
<213> Artificial Sequence

```

```

<220>
<221> ACETYLTATION
<222> 1

<221> MOD_RES
<222> 6
<223> Xaa is Leucine-therapeutic Agent

<223> conjugate

```

```

<400> 278
Gly Ser Gly Arg Ser Xaa
1          5

```

```

<210> 279
<211> 7
<212> PRT
<213> Artificial Sequence

```

```

<220>
<221> ACETYLTATION
<222> 1

```

-172-

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 279
Gly Ser Gly Arg Ser Ser Xaa
1 5

<210> 280
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 280
Gly Ser Gly Arg Xaa
1 5

<210> 281
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> AMIDATION
<222> 6

<221> MOD_RES
<222> 4
<223> Xaa is 4-Guanidino-phenylglycine

<223> conjugate

<400> 281
Gly Ser Gly Xaa Ser Leu
1 5

<210> 282
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION

-173-

<222> 1

<221> MOD_RES

<222> 7

<223> Cyclohexylamine-therapeutic Agent

<223> conjugate

<400> 282

Gly Ser Gly Arg Ser Ser Xaa
1 5

<210> 283

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 7

<223> Leucine-therapeutic agent

<223> conjugate

<400> 283

Gly Ser Gly Arg Ala Ser Xaa
1 5

<210> 284

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 6

<223> Nle-therapeutic agent

<223> conjugate

<400> 284

Gly Ser Gly Arg Ser Xaa
1 5

<210> 285

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<221> ACETYLATION

<222> (0)...(0)

-174-

<221> MOD_RES
<222> 6
<223> Nle-therapeutic agent

<223> conjugate

<400> 285
Gly Thr Gly Arg Ser Xaa
1 5

<210> 286
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> MOD_RES
<222> 1
<223> Succinyl-BALanine

<221> MOD_RES
<222> 6
<223> Nle-therapeutic Agent

<223> conjugate

<400> 286
Ala Thr Gly Arg Ser Xaa
1 5

<210> 287
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLTATION
<222> 1

<221> MOD_RES
<222> 6
<223> Cyclohexylalanine-therapeutic agent

<223> conjugate

<400> 287
Gly Thr Gly Arg Ser Xaa
1 5

<210> 288
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLTATION
<222> 1

-175-

<221> MOD_RES
<222> 2
<223> Xaa is Homoserine

<221> MOD_RES
<222> 6
<223> Nle-Therapeutic AgentNle

<223> conjugate

<400> 288
Gly Xaa Gly Arg Ser Xaa
1 5

<210> 289
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 2
<223> Xaa is D Serine

<221> MOD_RES
<222> 6
<223> Alanine-therapeutic Agent

<223> conjugate

<400> 289
Gly Xaa Ala Arg Ser Xaa
1 5

<210> 290
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 290
Gly Ser Ala Arg Ser Xaa
1 5

<210> 291
<211> 7

-176-

<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Cyclohexylalanine-therapeutic agent

<223> conjugate

<400> 291
Gly Ser Ala Arg Ser Ser Xaa
1 5

<210> 292
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 292
Gly Ser Ala Arg Ser Ser Xaa
1 5

<210> 293
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 293
Gly Ser Ala Arg Ala Ser Xaa
1 5

<210> 294
<211> 6
<212> PRT

-177-

<213> Artificial Sequence

<220>

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 6

<223> Leucine-therapeutic Agent

<223> conjugate

<400> 294

Val Ser Gly Arg Ser Xaa
1 5

<210> 295

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 6

<223> Leucine-therapeutic Agent

<223> conjugate

<400> 295

Val Ser Gly Arg Ala Xaa
1 5

<210> 296

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 7

<223> Leucine-therapeutic Agent

<223> conjugate

<400> 296

Val Ser Gly Arg Ala Ser Xaa
1 5

<210> 297

<211> 7

<212> PRT

<213> Artificial Sequence

-178-

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 297
Val Ser Gly Arg Ser Ser Xaa
1 5

<210> 298
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Alanine-therapeutic Agent

<223> conjugate

<400> 298
Val Ser Ala Arg Met Xaa
1 5

<210> 299
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 5
<223> Xaa is Nle

<221> MOD_RES
<222> 6
<223> Alanine-therapeutic Agent

<223> conjugate

<400> 299
Val Ser Ala Arg Xaa Xaa
1 5

<210> 300
<211> 6

-179-

<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Nle-therapeutic agent

<223> conjugate

<400> 300
Val Ser Ala Arg Ser Xaa
1 5

<210> 301
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 301
Val Ser Ala Arg Ser Xaa
1 5

<210> 302
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 1
<223> Xaa is S-Methylcysteine

<221> MOD_RES
<222> 6
<223> dValine-therapeutic Agent

<223> conjugate

<400> 302
Xaa Pro Gly Arg Val Xaa
1 5

-180-

<210> 303
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 1
<223> Xaa is S-Methylcysteine

<221> MOD_RES
<222> 6
<223> Valine-therapeutic Agent

<223> conjugate

<400> 303
Xaa Pro Gly Arg Val Xaa
1 5

<210> 304
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 1
<223> Xaa is S-Methylcysteine

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 304
Xaa Pro Gly Arg Ala Xaa
1 5

<210> 305
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 1
<223> Xaa is S-Methylcysteine

-181-

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 305
Xaa Pro Gly Arg Ser Xaa
1 5

<210> 306
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 1
<223> Xaa is S-Methylcysteine

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 306
Xaa Pro Ala Arg Ser Xaa
1 5

<210> 307
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 1
<223> Xaa is S-Methylcysteine

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 307
Xaa Pro Ala Arg Ala Ser Xaa
1 5

<210> 308
<211> 6

-182-

<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 1
<223> Xaa is t-Butyl Glycine

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 308
Xaa Pro Gly Arg Ser Xaa
1 5

<210> 309
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 3
<223> Xaa is D Serine

<221> MOD_RES
<222> 7
<223> Alanine-therapeutic Agent

<223> conjugate

<400> 309
Arg Gly Xaa Ala Arg Ser Xaa
1 5

<210> 310
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Alanine-therapeutic Agent

<223> conjugate

-183-

<400> 310
Arg Gly Ser Gly Arg Ser Xaa
1 5

<210> 311
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLTATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 311
Arg Gly Ser Gly Arg Ala Xaa
1 5

<210> 312
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLTATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 312
Arg Gly Ser Gly Arg Ser Xaa
1 5

<210> 313
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLTATION
<222> 1

<221> MOD_RES
<222> 7
<223> Nle-therapeutic agent

<223> conjugate

<400> 313

-184-

Arg Gly Ser Gly Arg Ser Xaa
1 5

<210> 314
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Nle-therapeutic agent

<223> conjugate

<400> 314
Arg Gly Ser Gly Arg Ala Xaa
1 5

<210> 315
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 315
Arg Gly Ser Gly Arg Ser Ser Xaa
1 5

<210> 316
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Cyclohexylalanine-therapeutic agent

<223> conjugate

<400> 316
Arg Gly Ser Gly Arg Ser Xaa

-185-

1 5

<210> 317
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Cyclohexylalanine-therapeutic agent

<223> conjugate

<400> 317
Arg Gly Ser Gly Arg Ser Ser Xaa
1 5

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<223> conjugate

<400> 318
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<221> MOD_RES
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<223> conjugate

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<221> MOD_RES
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<223> conjugate

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<223> conjugate

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<223> conjugate

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<222> 8
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<223> conjugate

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<223> conjugate

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<223> conjugate

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<223> conjugate

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<223> conjugate

<400> 342
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1 5

-194-

<210> 343
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<223> conjugate

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<223> conjugate

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<223> conjugate

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<223> conjugate

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Val Ile Val Ser Ala Arg Ser Xaa
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1 5

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Ser Gly Arg Ser Ser Xaa

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1 5

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1 5

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Thr Gly Arg Ser Xaa
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<223> conjugate

<400> 380

Thr Gly Arg Ser Xaa
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<210> 381

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<223> Abu-therapeutic agent

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Thr Gly Arg Thr Xaa
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Thr Gly Arg Xaa Xaa
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<223> conjugate

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Thr Gly Arg Xaa Xaa
1 5

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<400> 384
Thr Gly Arg Xaa Xaa
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<223> conjugate

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Thr Gly Xaa Ser Xaa
1 5

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<400> 386
Thr Gly Xaa Ser Xaa
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Thr Gly Xaa Xaa Xaa
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<223> Xaa is Alloc

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Thr Gly Xaa Ser Xaa
1 5

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Thr Gly Lys Ser Xaa
1 5

-210-

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<223> conjugate

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Xaa Gly Arg Ser Xaa
1 5

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<223> Nle-therapeutic agent

<223> conjugate

<400> 392

Xaa Gly Arg Ser Xaa
1 5

<210> 393

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<223> conjugate

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Xaa Gly Arg Ser Xaa
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<221> MOD_RES
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<223> Nle-therapeutic agent

<223> conjugate

<400> 395
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<212> PRT
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<221> MOD_RES
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<223> conjugate

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Xaa Gly Arg Ser Xaa
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<223> conjugate

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Xaa Gly Arg Ser Xaa
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<223> Xaa is 2-Pyridin-2-yl-acetyl threonine

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<223> Nle-therapeutic agent

<223> conjugate

<400> 398

Xaa Gly Arg Ser Xaa

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<210> 399

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<223> conjugate

<400> 399

Xaa Gly Arg Ser Xaa

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threonine

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<223> Nle-therapeutic agent

<223> conjugate

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Thr Gly Arg Ser Xaa

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<220>
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<221> MOD_RES
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<223> conjugate

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<223> conjugate

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<223> conjugate

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<213> Artificial Sequence

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<221> MOD_RES

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<223> conjugate

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<210> 405

<211> 5

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<223> Nle-therapeutic agent

<223> conjugate

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Thr Gly Arg Ser Xaa
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<223> Nle-therapeutic agent

<223> conjugate

<400> 406

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<211> 5
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<223> conjugate

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<210> 410
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<223> conjugate

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<210> 413
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<223> conjugate

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<223> conjugate

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<223> conjugate

<400> 418

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<400> 419

Thr Ala Arg Xaa Xaa

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<210> 420

<211> 5

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<223> Abu-therapeutic agent

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<400> 420

Thr Ala Arg Ser Xaa

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<223> conjugate

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<223> Xaa is 1-Methyl histidine

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<223> Nle-therapeutic agent

<223> conjugate

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<223> Xaa is 3-Methyl histidine

<221> MOD_RES

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<223> Nle-therapeutic agent

<223> conjugate

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<223> Xaa is Abu

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<223> Cyclohexyl alanine-therapeutic agent

<223> conjugate

<400> 434

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<223> conjugate

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Xaa Arg Ser Xaa

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<223> conjugate

<400> 444

Xaa Arg Ser Xaa

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Gln Gly Arg Ser Xaa
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Asn Gly Arg Ser Ser Xaa

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Gln Xaa Arg Ser Ser Xaa
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<221> ACETYLATION
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<221> MOD_RES
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<223> Xaa is Cyclohexylalanine

<221> MOD_RES
<222> 6
<223> Cyclohexylalanine-therapeutic agent

<400> 465
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1 5

<210> 466

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<211> 5
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<223> Leucine-therapeutic agent

<400> 466
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1 5

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Gln Phe Arg Ser Ser Xaa
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<210> 469
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<223> Cyclohexylalanine-therapeutic agent

<400> 472

Arg Gly Arg Ser Xaa
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<223> Leucine-therapeutic agent

<400> 473

Arg Ala Arg Ser Xaa
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<400> 474

Arg Ala Arg Ser Ser Xaa
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<400> 480
Arg Phe Arg Ser Xaa
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<221> ACETYLATION

<222> 1

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<222> 6

<223> Leucine-therapeutic agent

<400> 481

Tyr Gly Arg Ser Ser Xaa
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<211> 5

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<221> ACETYLATION

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<221> MOD_RES

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<223> Leucine-therapeutic agent

<400> 482

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<211> 5

<212> PRT

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<221> MOD_RES

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<223> Xaa is Methoxycarbonyl-(alpha-(3-cyanobenzyl))
glutamic acid-delta-methyl ester

<221> AMIDATION

<222> 5

<400> 483

Xaa Gly Arg Ser Leu
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<210> 484

<211> 5

<212> PRT

<213> Artificial Sequence

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<220>
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<221> MOD_RES
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glutamic acid -delta-methyl ester

<221> AMIDATION
<222> 5

<400> 484
Xaa Gly Arg Ser Leu
1 5

<210> 485
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<221> MOD_RES
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(alpha-(3-amidinobenzyl)) glutamic acid

<221> AMIDATION
<222> 5

<400> 485
Xaa Gly Arg Ser Leu
1 5

<210> 486
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<221> MOD_RES
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)glutamic acid -delta-methyl ester

<221> AMIDATION
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<400> 486
Xaa Gly Arg Ser Leu
1 5

<210> 487
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<213> Artificial Sequence

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(alpha-(3-methylbenzyl)) glutamic acid

<221> AMIDATION

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Xaa Gly Arg Ser Leu
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<223> Xaa is Methoxycarbonyl-(alpha-(3-methylbenzyl)
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<221> MOD_RES

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<223> Leucine-therapeutic agent

<400> 489

Xaa Gly Arg Ser Xaa
1 5

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<210> 490
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glutamic acid -delta-methyl ester

<221> MOD_RES
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Xaa Gly Arg Ser Xaa
1 5

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1 5

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1 5

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<400> 494
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<210> 496

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<211> 6
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<223> dNle-therapeutic agent

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Arg Gln Ala Arg Ala Xaa

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<223> Nva-therapeutic agent

<400> 513

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<210> 514

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<400> 526
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<400> 528
Arg Gln Ser Arg Ser Xaa
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<400> 529

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Arg Gln Ser Arg Thr Xaa
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<222> 7
<223> Leucine-therapeutic agent

<400> 530
Arg Gln Thr Arg Ser Ser Xaa
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<400> 531
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<400> 532
Arg Asn Ser Arg Ser Xaa

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<400> 533
Arg Gln Phe Arg Ser Xaa
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<400> 534
Arg Gln Phe Arg Ser Xaa
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<210> 535
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<222> 6
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<400> 535
Arg Gln Phe Arg Ser Xaa
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<210> 536
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<400> 536
Arg Gln Phe Arg Ser Xaa
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Arg Gln Phe Arg Ser Xaa
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<400> 538
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<400> 543
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<221> MOD_RES

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<213> Artificial Sequence

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<221> MOD_RES

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1 5

<210> 592
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<220>
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<221> MOD_RES
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<400> 598
Xaa Xaa Arg Ser Xaa
1 5

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<221> MOD_RES
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<223> Leucine-therapeutic agent

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Xaa Xaa Arg Ser Xaa
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<210> 601

<211> 6

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<222> 6

<223> Leucine-therapeutic agent

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<221> MOD_RES

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<223> Xaa is Methoxycarbonyl-(alpha)-3-methylbenzyl
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<221> MOD_RES

<222> 5

<223> Leucine-therapeutic agent

<400> 604

Xaa Gly Arg Ser Xaa

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<223> Xaa is D-cyclohexylalanine

<221> MOD_RES

<222> 2

<223> Xaa is 4Hyp

<221> MOD_RES

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<220>
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glutamic acid -delta-methyl ester

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<400> 608
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glutamic acid

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<220>
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Leu Arg Arg Gln Ser Arg Ala Xaa
1 5